

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: May 22, 2002, 15:37:06 ; Search time 13.4 Seconds  
(Without alignments) 944.873 Million cell updates/sec

Title: US-09-771-209-76

Perfect score: 1687  
Sequence: 1 MERRHSGVSEFVLGFPF.....RTLHLAQDEANTKNGSKIG 327

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1680	99.6	327	1	OLF7_RAT
2	1432	84.9	327	1	06A1_HUMAN
3	957.5	56.8	311	1	06B1_HUMAN
4	788	46.7	311	1	OLF6_RAT
5	751	44.5	222	1	OLF6_MOUSE
6	719.5	42.6	317	1	0A45_HUMAN
7	711.5	42.2	321	1	05V1_HUMAN
8	710.5	42.0	315	1	0A44_HUMAN
9	709	42.0	312	1	0A41_HUMAN
10	697.5	41.3	315	1	0B41_HUMAN
11	688.5	40.8	314	1	05F1_HUMAN
12	671	39.8	316	1	02H3_HUMAN
13	670	39.7	357	1	02B2_HUMAN
14	669	39.7	312	1	02H2_HUMAN
15	667	39.5	313	1	02B6_HUMAN
16	665	39.4	313	1	02B3_HUMAN
17	663	39.3	311	1	OLF1_CANFA
18	662.5	39.3	313	1	OLF5_RAT
19	659.5	39.1	314	1	05I1_HUMAN
20	656	38.9	319	1	02S2_HUMAN
21	653.5	38.7	320	1	07G1_HUMAN
22	650.5	38.6	311	1	OLF2_CANFA
23	650.5	38.6	313	1	01C1_HUMAN
24	649	38.5	308	1	02D2_HUMAN
25	644	38.2	312	1	01L5_MOUSE
26	644	38.2	318	1	0A41_HUMAN
27	642.5	38.1	314	1	0A43_HUMAN
28	640	37.9	315	1	0A43_HUMAN
29	638	37.8	316	1	02H1_HUMAN
30	636.5	37.7	313	1	OLF2_CANFA
31	636	37.7	320	1	0A41_HUMAN
32	635	37.6	314	1	OLF1_RAT
33	634.5	37.6	312	1	02J2_HUMAN

34	632.5	37.5	312	1	OLF1_HUMAN	043749 homo sapien
35	631	37.4	315	1	0A42_HUMAN	060403 homo sapien
36	629	37.3	317	1	02F1_HUMAN	013607 homo sapien
37	628.5	37.3	320	1	07C2_HUMAN	060412 homo sapien
38	627.5	37.2	311	1	02J3_HUMAN	076001 homo sapien
39	627	37.2	317	1	OLF3_CANFA	095156 canis fami
40	626.5	37.1	313	1	01G1_HUMAN	P47890 homo sapien
41	625	37.0	312	1	OLF4_RAT	P23273 rattus norv
42	624	37.0	309	1	01A1_HUMAN	Q9P145 homo sapien
43	623	36.9	312	1	02C1_HUMAN	Q95371 homo sapien
44	623	36.9	314	1	01E1_HUMAN	P30953 homo sapien
45	621.5	36.8	307	1	0CD2_HUMAN	P58182 homo sapien

## ALIGNMENTS

RESULT	ID	STANDARD	PRT	MA
1	OLF7_RAT			327 AA.
AC	P23270			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	01-JUL-1993 (Rel. 26, Last annotation update)			
DE	olfactory receptor-like protein 17.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91191556; PubMed=1840504;			
RA	Buck L., Axel R.;			
RT	"A novel multigene family may encode odorant receptors: a molecular			
RT	basis for odor recognition."			
RL	Cell 65:175-187(1991).			
CC	-1- FUNCTION: PUTATIVE ODORANT RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
DR	EMBL; M64386; AAA41749.1; -			
DR	PIR; F23701; F23701.			
DR	GCRDB; GCR_0148; -			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00245; OLFACTORYR.			
DR	PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.			
DR	PROSITE; PS50262; G-PROTEIN_RECEP_FL_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Multigene family; Olfaction.			
FT	DOMAIN 1			
FT	TRANSMEM 27			
FT	TRANSMEM 51			
FT	TRANSMEM 59			
FT	TRANSMEM 81			
FT	DOMAIN 105			
FT	TRANSMEM 125			
FT	DOMAIN 126			
FT	TRANSMEM 144			
FT	TRANSMEM 145			
FT	DOMAIN 164			
FT	TRANSMEM 201			
FT	TRANSMEM 202			
FT	TRANSMEM 224			
FT	DOMAIN 225			
FT	TRANSMEM 241			
FT	TRANSMEM 242			
FT	DOMAIN 266			
FT	TRANSMEM 277			
FT	TRANSMEM 278			
FT	TRANSMEM 297			
FT	TRANSMEM 7 (POTENTIAL).			

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FT DOMAIN 298 327 CYTOPLASMIC (POTENTIAL).
FT CAROHD 5 5 N-LINKED (GLCNMC. . .) (POTENTIAL).
FT DISULFID 102 194 BY SIMILARITY.
SQ SEQUENCE 327 AA: 36265 MW: 85863DE961621D9 CRC64:

Query Match
Best Local Similarity 99.7%; Score 1680; DB 1; Length 327;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MERRNSGRVSEFVLLGFPAPAPARLVLFELSLDYLVLTENMLIIAIRNHTLHKPM 60
DB 1 MERRNSGRVSEFVLLGFPAPAPARLVLFELSLDYLVLTENMLIIAIRNHTLHKPM 60
OY 61 YFFLANMSFLEIYVTVITPKMLAGFTSGKENHGOLISEPACTOLYFFLGICTECVLL 120
DB 61 YFFLANMSFLEIYVTVITPKMLAGFTSGKENHGOLISEPACTOLYFFLGICTECVLL 120
OY 121 AYMAVDYVAICHPPLHYPIYVSRLCVQMAAGSMAGGFGISMKVPLISRLSYCGPNTIN 180
DB 121 AYMAVDYVAICHPPLHYPIYVSRLCVQMAAGSMAGGFGISMKVPLISRLSYCGPNTIN 180
OY 181 HFFCDVSPLLNSTCTDMSTAEITDFVLAIFILLGPLSVTGASYMATGAVMRIPSAAGR 240
DB 181 HFFCDVSPLLNSTCTDMSTAEITDFVLAIFILLGPLSVTGASYMATGAVMRIPSAAGR 240
OY 241 KAFSTCASHLVTVITFYASIFLYARPKALSAFDTKLVSVLYAVLPFNPIIYCLRNQ 300
DB 241 KAFSTCASHLVTVITFYASIFLYARPKALSAFDTKLVSVLYAVLPFNPIIYCLRNQ 300
OY 301 DVKRALRRTLHLAODEANTNKGSKIG 327
DB 301 DVKRALRRTLHLAODEANTNKGSKIG 327

RESULT 2
O6A1_HUMAN STANDARD: PRT: 327 AA.
ID 06A1_HUMAN STANDARD: PRT: 327 AA.
AC 095222:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 6A1 (Olfactory receptor 11-55) (OR11-55).
GN OR6A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99005533; PubMed=9787077;
RA Buettner J.A., Glusman G., Ben-Arie N., Ramos P., Lancel D.,
RA Evans G.A.;
RT "Organization and evolution of olfactory receptor genes on human
RT chromosome 11."
RL Genomics 53:56-68(1998).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF065870; AAC70018.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECER_FL_1; FALSE_NEG.

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DR PROSITE: PS00262; G_PROTEIN_RECER_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 26
FT TRANSMEM 27 50
FT DOMAIN 51 58
FT TRANSMEM 59 80
FT TRANSMEM 81 105
FT DOMAIN 106 125
FT TRANSMEM 126 144
FT TRANSMEM 145 163
FT TRANSMEM 164 201
FT TRANSMEM 202 224
FT TRANSMEM 225 241
FT TRANSMEM 242 264
FT TRANSMEM 265 277
FT TRANSMEM 278 297
FT DOMAIN 298 320
FT DISULFID 102 194
FT CAROHD 5 5
FT CAROHD 191 191
SQ SEQUENCE 327 AA: 36049 MW: 69956A573BCFDA04 CRC64:

Query Match
Best Local Similarity 84.9%; Score 1432; DB 1; Length 327;
Matches 281; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

OY 1 MERRNSGRVSEFVLLGFPAPAPARLVLFELSLDYLVLTENMLIIAIRNHTLHKPM 60
DB 1 MERRNSGRVSEFVLLGFPAPAPARLVLFELSLDYLVLTENMLIIAIRNHTLHKPM 60
OY 61 YFFLANMSFLEIYVTVITPKMLAGFTSGKENHGOLISEPACTOLYFFLGICTECVLL 120
DB 61 YFFLANMSFLEIYVTVITPKMLAGFTSGKENHGOLISEPACTOLYFFLGICTECVLL 120
OY 121 AYMAVDYVAICHPPLHYPIYVSRLCVQMAAGSMAGGFGISMKVPLISRLSYCGPNTIN 180
DB 121 AYMAVDYVAICHPPLHYPIYVSRLCVQMAAGSMAGGFGISMKVPLISRLSYCGPNTIN 180
OY 181 HFFCDVSPLLNSTCTDMSTAEITDFVLAIFILLGPLSVTGASYMATGAVMRIPSAAGR 240
DB 181 HFFCDVSPLLNSTCTDMSTAEITDFVLAIFILLGPLSVTGASYMATGAVMRIPSAAGR 240
OY 241 KAFSTCASHLVTVITFYASIFLYARPKALSAFDTKLVSVLYAVLPFNPIIYCLRNQ 300
DB 241 KAFSTCASHLVTVITFYASIFLYARPKALSAFDTKLVSVLYAVLPFNPIIYCLRNQ 300
OY 301 DVKRALRRTLHLAODEANTNKGSK 325
DB 301 DVKRALRRTLHLAODEANTNKGSK 325

RESULT 3
O6B1_HUMAN STANDARD: PRT: 311 AA.
ID 06B1_HUMAN STANDARD: PRT: 311 AA.
AC 095007:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 6B1 (Olfactory receptor 7-3) (OR7-3).
GN OR6B1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Bauer C., Williams D.;
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----
DR EMBL: AC004853; AAC64377.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1.1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_REC_P1.1; 1.
DR PROSITE: PS50262; G-PROTEIN_REC_P1.2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family; Olfaction.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 49 1 (POTENTIAL).
FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 79 2 (POTENTIAL).
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 120 3 (POTENTIAL).
FT DOMAIN 121 139 4 (POTENTIAL).
FT TRANSMEM 140 158 4 (POTENTIAL).
FT DOMAIN 159 195 5 (POTENTIAL).
FT TRANSMEM 196 219 5 (POTENTIAL).
FT DOMAIN 220 234 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 235 257 6 (POTENTIAL).
FT DOMAIN 258 270 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 271 290 7 (POTENTIAL).
FT DOMAIN 291 311 CYTOPLASMIC (POTENTIAL).
FT DISULFID 97 189 BY SIMILARITY.
FT CARBOHYD 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 311 AA; 35299 MW; 67LFD19658FE0616 CRC64;

Query Match 56.8%; Score 957.5; DB 1; Length 311;
Best Local Similarity 56.8%; Pred. No. 5e-67;
Matches 175; Conservative 54; Mismatches 72; Indels 7; Gaps 3;

OY 1 MERRNHGVSFEVLLGPPAPAPLRLVLLFSLLDVYLVTENMLIIAIRNHPPLHKRM 60
DB 1 MELENOT-RVTKFLLVFGPGLSRAAMPFLPLVAVILVANVNIILLVQNRPLHKRM 59
OY 61 YFFLANMSTLEIVYVTRIPKMLAGFISGENHGOILSEACMTQLPFLGLGCTBCVLL 120
DB 60 YFFLANMSTLEIVYVTRIPKMLAGFISGENHGOILSEACMTQLPFLGLGCTBCVLL 115
OY 121 AVMAVDYVAICHPPIYVIVSRLCVOMAGSMAGFGISWVKVFLISRLSYCGPNTIN 180
DB 116 AAMAYDRYVAICRPLHPIYVIVSRLCVOMAGSMAGFGISWVKVFLISRLSYCGPNTIN 175
OY 181 HFFCDVSPILNSCTDMSTAEFLDFVLAIFLLGPLSVTGASYMAITGAVMRIPSAAGR 240
DB 176 HFFCDISPILNSCTDMSTAEFLDFVLAIFLLGPLSVTGASYMAITGAVMRIPSAAGR 240
OY 241 KAFSCASHLVYVIVFVYASIFIVAPKRLSAFDENKIVSVLYAVIFNFIYICLRQ 300
DB 234 KAFSCASHLVYVIVFVYASIFIVAPKRLSAFDENKIVSVLYAVIFNFIYICLRQ 300
OY 301 DVKRALRR 308
DB 294 EVKALKK 301

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DE Olfactory receptor-like protein F6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91191556; PubMed=1840504;
RA Buck L., Axel R.;
RT "A novel multigene family may encode odorant receptors: a molecular
RT basis for odor recognition.";
RL Cell 65:175-187(1991).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: M64378; AAA41741.1; -
DR PIR: C23701; C23701.
DR GCRDB: GCR_0146; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1.1.
DR PRINTS: PR00245; OLFACTORYR.
DR PROSITE: PS00237; G-PROTEIN_REC_P1.1; 1.
DR PROSITE: PS50262; G-PROTEIN_REC_P1.2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family; Olfaction.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 53 1 (POTENTIAL).
FT DOMAIN 54 60 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 61 82 2 (POTENTIAL).
FT DOMAIN 83 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 123 3 (POTENTIAL).
FT DOMAIN 124 142 4 (POTENTIAL).
FT TRANSMEM 143 161 4 (POTENTIAL).
FT DOMAIN 162 199 5 (POTENTIAL).
FT TRANSMEM 200 222 5 (POTENTIAL).
FT DOMAIN 223 239 6 (POTENTIAL).
FT TRANSMEM 240 263 6 (POTENTIAL).
FT DOMAIN 264 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 295 7 (POTENTIAL).
FT DOMAIN 296 311 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 100 192 BY SIMILARITY.
SQ SEQUENCE 311 AA; 34168 MW; 9E092CFE85A58BF1 CRC64;

Query Match 46.7%; Score 788; DB 1; Length 311;
Best Local Similarity 50.7%; Pred. No. 5.8e-54;
Matches 151; Conservative 46; Mismatches 97; Indels 4; Gaps 1;

OY 13 FVLGFPAPAPLRLVLLFSLLDVYLVTENMLIIAIRNHPPLHMPYFPLANNSPLEI 72
DB 15 FILLGFPAPAPLRLVLLFSLLDVYLVTENMLIIAIRNHPPLHMPYFPLANNSPLEI 74
OY 73 WYVYVTRIPKMLAGFISGENHGOILSEACMTQLPFLGLGCTBCVLLAVMAVDYVAIC 132
DB 75 WYVYVTRIPKMLAGFISGENHGOILSEACMTQLPFLGLGCTBCVLLAVMAVDYVAIC 130
OY 133 HPLHPIYVIVSRLCVOMAGSMAGFGISWVKVFLISRLSYCGPNTINHFCDVSPILNL 192
DB 131 LPLRIGGIMTGPLAMRLAGSLGFSATYVATILARSLFGSKRVINHFCDISPATVL 190
OY 193 SCTDMSTAEFLDFVLAIFLLGPLSVTGASYMAITGAVMRIPSAAGRKAFTSCASHLV 252
DB 193 SCTDMSTAEFLDFVLAIFLLGPLSVTGASYMAITGAVMRIPSAAGRKAFTSCASHLV 252

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ID	Sequence	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232	Score	DB 233	Length	DB 234	Score	DB 235	Length	DB 236	Score	DB 237	Length	DB 238	Score	DB 239	Length	DB 240	Score	DB 241	Length	DB 242	Score	DB 243	Length	DB 244	Score	DB 245	Length	DB 246	Score	DB 247	Length	DB 248	Score	DB 249	Length	DB 250	Score	DB 251	Length	DB 252	Score	DB 253	Length	DB 254	Score	DB 255	Length	DB 256	Score	DB 257	Length	DB 258	Score	DB 259	Length	DB 260	Score	DB 261	Length
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DB	1	YELTSMSELEANYISVTPYKMLAGFL---	HPNPNTISFLGCGTQLYLFPMSLACFCBCVLLA	56
QY	122	WAATRYAIAICHPRLPIVPIVSRLCVQMAAGSAGAGFCIGSMVKVPLISRLSCGPNNTNH	181	
DB	57	AAAYRYAIAICHPRLPIVPIVSRLCVQMAAGSAGAGFCIGSMVKVPLISRLSCGPNNTNH	116	
QY	182	FFCDVSPPLNLSCTQMSMAETLDFVLAIFILLGPLSPVSGASYMAATGAVMRIPSAAGRHK	241	
DB	117	FFCDVSPPLNLSCTQMSMAETLDFVLAIFILLGPLSPVSGASYMAATGAVMRIPSAAGRHK	176	
QY	242	AFTSCASHLTWVITFIYAASIFIYAPPKALSAFDTKKLVSLYAV	285	
DB	177	AFTSCASHLTWVITFIYAASIFIYAPPKALSAFDTKKLVSLYAV	220	
RESULT	5			
OAA5_HUMAN		STANDARD:	PRT:	317 AA.
AC	Q9H207:			
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	01-MAR-2002	(Rel. 41, Last annotation update)		
DE	Olfactory receptor 10A5 (H3) (Putative taste receptor JG66).			
GN	OR10A5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Lane R.P., Culforth T., Young J., Athanasios M., Friedman C.,			
RA	Roven L., Evans G., Axel R., Hood L., Trask B.J.;			
RT	"Genomic analysis of orthologous mouse and human olfactory receptor			
RT	loci indicates cluster stability yet minimal conservation beyond the			
RT	coding sequence.";			
RL	Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Tongue;			
RX	MEDLINE=21562400; PubMed=11705801;			
RA	Gaudin J.C., Breuils L., Haerle T.;			
RT	"New GPCRs from a human lingual cDNA library.";			
RL	Chem. Senses 26:1157-1166(2001).			
CC	-!- FUNCTION: PUTATIVE ODORANT RECEPTOR.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL: AF321237; AAG45206.1; -			
DR	EMBL: AF324499; AAI33005.1; -			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	Pfam: PF00001; 7tm_1; 1.			
DR	PRINTS: PR00237; GPCR_RHODOPSIN.			
DR	PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.			
DR	PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Multigene family; Olfaction.			
FT	DOMAIN	1	26	
FT	TRANSMEM	27	30	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	51	58	1 (POTENTIAL).
FT	TRANSMEM	59	80	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	81	101	2 (POTENTIAL).
FT	TRANSMEM	102	121	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	122	140	3 (POTENTIAL).
FT	TRANSMEM	141	159	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	160	196	4 (POTENTIAL).
FT	DOMAIN			EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 197 220 5 (POTENTIAL).  
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 238 260 6 (POTENTIAL).  
 FT DOMAIN 261 273 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 274 293 7 (POTENTIAL).  
 FT DOMAIN 294 317 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 98 190 BY SIMILARITY.  
 FT CARBOHYD 5 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 317 AA; 35519 MW; 464073EFC4ECSB45 CRC64;

Query Match 42.6%; Score 719.5; DB 1; Length 317;  
 Best Local Similarity 46.9%; Pred. No. 1.1e-48;  
 Matches 142; Conservative 48; Mismatches 108; Indels 5; Gaps 2;

QY 10 VSEFVLGPPA-PAPRLVLFLLSDYVLTENMLIIAIRNPTLHKPFYFLANKS 68  
 DB 9 ISEFLMSESSLPTEIOSLFTFLTYLVTLKNSLIIVTLADPMLHSPPYFELRNLS 68  
 QY 69 FLEIYVVTIPKMLAGFSGKENHGOISFEACMTOLYFELGLCTECVLLAVMAVDREY 128  
 DB 69 FLEIFNLIYVYKMLGTLLAODT-----ISFLGCATOMTEFFFEFGVACFLLATMAVDREY 124  
 QY 129 VAICPHLPVIVSSRLCVQMAAGSGAGFGISMWKVELISRLSYCPNTINHFCQVSP 188  
 DB 125 VAICSPHLPVIMORTAKLAAASMPFGPVAQTWTMLFSFPGCTNKNVHFCQDSP 184  
 QY 189 LLNLSTDMSTAEITDPAVLAIFILGLPSVTCASMAITGAVMRIPSAAGRKASTCS 248  
 DB 185 VKLVLCAPTALEIYAIYGLTVLWMPCLLISYTRIAALIKIPSAAGRKASTCS 244  
 QY 249 HLTVIIFEYASIFIYAPRKALSAFDTKLVSVLAVIPLFNPITLYCLRNODVRAALRR 308  
 DB 245 HLTVSLFETISSLTYPFKSPNSPESKLLSLSTVYTPMLNPITLYSLRSEVANALSR 304  
 QY 309 TLH 311  
 DB 305 TFH 307

RESULT 7  
 05V1\_HUMAN STANDARD; PRT; 321 AA.  
 AC 09GFG6:  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Olfactory receptor 5V1 (Hs6M1-21).  
 GN OR5V1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN NCI  
 RP SEQUENCE FROM N.A.  
 RA Tracey A.;  
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC EMBL: AL096770; CAB65797.1;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODOPSN.

DR PROSITE: PS00237; G-PROTEIN\_REC\_P1.1;  
 DR PROSITE: PS00262; G-PROTEIN\_REC\_P1.2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Olfaction.  
 FT TRANSMEM 1 25 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 26 49 1 (POTENTIAL).  
 FT TRANSMEM 50 57 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 58 79 2 (POTENTIAL).  
 FT TRANSMEM 80 100 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 101 120 3 (POTENTIAL).  
 FT TRANSMEM 121 139 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 140 158 4 (POTENTIAL).  
 FT TRANSMEM 159 195 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 196 219 5 (POTENTIAL).  
 FT TRANSMEM 220 236 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 237 259 6 (POTENTIAL).  
 FT TRANSMEM 260 272 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 273 292 7 (POTENTIAL).  
 FT TRANSMEM 293 321 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 97 189 BY SIMILARITY.  
 FT CARBOHYD 5 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 321 AA; 36056 MW; AAC426FDC58E375 CRC64;

Query Match 42.2%; Score 711.5; DB 1; Length 321;  
 Best Local Similarity 45.9%; Pred. No. 4.7e-48;  
 Matches 141; Conservative 56; Mismatches 105; Indels 5; Gaps 2;

QY 1 MERRNHSGRVSEFVLGPPAPRLVLFLLSDYVLTENMLIIAIRNPTLHKPM 60  
 DB 1 MERKQTA-ITFEIILGFSNLELOFLFTIFLTYFCTGLGNILITVTDPHLP 59  
 QY 61 YEFLLNMSLEIYVVTIPKMLAGFSGKENHGOISFEACMTOLYFELGLCTECVLL 120  
 DB 60 YFELGLAEITDICTYTSNPPQMMVHLSKRKS----ISYGCVQVQFAFVFEVSSCLL 115  
 QY 121 AVMAVDYVAICPHLPVIVSSRLCVQMAAGSGAGFGISMWKVELISRLSYCPNTIN 180  
 DB 116 AVMAVDYVAICPHLPVIVSSRLCVQMAAGSGAGFGISMWKVELISRLSYCPNTIN 175  
 QY 181 HFCQVSPLLNLCSTDMSTAEITDPAVLAIFILGLPSVTCASMAITGAVMRIPSAAGR 240  
 DB 176 YFCQDIPLLILSCGWTGVTNELLALSTGVETGTPCLIVSLICITSLRLQSEGR 225  
 QY 241 KAFSTCASLHYIYFIYASIFIYAPRKALSAFDTKLVSVLAVIPLFNPITLYCLRNQ 300  
 DB 236 KAFSTCASLHYIYFIYASIFIYAPRKALSAFDTKLVSVLAVIPLFNPITLYCLRNQ 295  
 QY 301 DVKRALR 307  
 DB 296 DIKEAVK 302

RESULT 8  
 0AA4\_HUMAN STANDARD; PRT; 315 AA.  
 AC 09H209:  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Olfactory receptor 10A4 (HP2).  
 GN OR10A4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN NCI  
 RP SEQUENCE FROM N.A.  
 RA Lane R.P., Cutforth T., Young J., Athanasios M., Friedman C.,  
 RA Rowen U., Evans G., Axel R., Hood L., Trask B.J.;  
 RT "Genomic analysis of orthologous mouse and human olfactory receptor  
 RT loci indicates cluster stability yet minimal conservation beyond the  
 RT coding sequence.";

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 CC - FUNCTION: PUTATIVE ODORANT RECEPTOR.  
 CC - SUBCELLULAR LOCATION: Integral membrane protein.  
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL: AF321237; AAC45205.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHOOPSN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Olfaction.  
 FT DOMAIN 1 26  
 FT TRANSMEM 27 50  
 FT DOMAIN 51 58  
 FT TRANSMEM 59 80  
 FT DOMAIN 81 101  
 FT TRANSMEM 102 121  
 FT DOMAIN 122 140  
 FT TRANSMEM 141 159  
 FT DOMAIN 160 196  
 FT TRANSMEM 197 220  
 FT DOMAIN 221 237  
 FT TRANSMEM 238 260  
 FT DOMAIN 261 273  
 FT TRANSMEM 274 293  
 FT DOMAIN 294 315  
 FT DISULFID 98 190  
 FT CARBOHYD 5  
 SQ SEQUENCE 315 AA; 35100 MW; 68DF6780CA8004A CRC64;  
 N-LINKED (GLCNAC... ) (POTENTIAL).  
 Query Match 42.1%; Score 710.5; DB 1; Length 315;  
 Best Local Similarity 46.9%; Pred. No. 5.5e-48;  
 Matches 142; Conservative 47; Mismatches 109; Indels 5; Gaps 2;

AC 096KK4;  
 DT 01-MAR-2002 (Rel. 41, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Olfactory receptor 10C1 (Hs6M1-17).  
 GN OR10C1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Whitaker H.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 CC - FUNCTION: PUTATIVE ODORANT RECEPTOR.  
 CC - SUBCELLULAR LOCATION: Integral membrane protein.  
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL: AL035542; CAB44507.1; ALT\_INIT.  
 DR PROSITE: PS00237; G-PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Olfaction.  
 FT DOMAIN 1 24  
 FT TRANSMEM 25 48  
 FT DOMAIN 49 56  
 FT TRANSMEM 57 78  
 FT DOMAIN 79 99  
 FT TRANSMEM 100 119  
 FT DOMAIN 120 138  
 FT TRANSMEM 139 157  
 FT DOMAIN 158 194  
 FT TRANSMEM 195 218  
 FT DOMAIN 219 235  
 FT TRANSMEM 236 258  
 FT DOMAIN 259 271  
 FT TRANSMEM 272 291  
 FT DOMAIN 292 312  
 FT DISULFID 96 188  
 FT CARBOHYD 4  
 SQ SEQUENCE 312 AA; 34351 MW; B6FD6E0E700CB2CC CRC64;  
 N-LINKED (GLCNAC... ) (POTENTIAL).  
 Query Match 42.0%; Score 709; DB 1; Length 312;  
 Best Local Similarity 46.6%; Pred. No. 7.1e-48;  
 Matches 142; Conservative 49; Mismatches 110; Indels 4; Gaps 1;



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CC EMBL: AF065863; AAC70017.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_REC_F1_1; FALSE_NEG.
DR PROSITE: PS50262; G_PROTEIN_REC_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family; Olfaction.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 49 1 (POTENTIAL).
FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 79 2 (POTENTIAL).
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 120 3 (POTENTIAL).
FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 158 4 (POTENTIAL).
FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 196 219 5 (POTENTIAL).
FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 237 259 6 (POTENTIAL).
FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 273 292 7 (POTENTIAL).
FT DOMAIN 293 314 CYTOPLASMIC (POTENTIAL).
FT DISULFID 314 314 BY SIMILARITY.
FT CARBOHYD 97 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 314 AA; 35131 MW; C14A9A35CD76E3A3 CRC64;

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Query Match 40.8%; Score 688.5; DB 1; Length 314;
Best Local Similarity 43.9%; Pred. No. 2.7e-46;
Matches 136; Conservative 60; Mismatches 109; Indels 5; Gaps 2;

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OY 1 MERRHNSGVSEVLLGFPAPAPRLVLFLLSLDVLVLTETMLITIRNHPPLHKPM 60
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 1 MRRKNTS-LTEFVLGLADTELEQITLFLPLVITLVVGLSGMILLIRIDSOATHRM 59
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 61 YFFLANMSFLEITWYVTVTIPKMLAGFIGSKENHGQISFACMTQVFLGLGCECVLL 120
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 60 YFFLANLSFVDCNSTTTPKMLADLSEKKT---ISFAGCEFLQWYFISLATTECILF 115
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 121 AVMADRYVAICHPPLHYPIVVSRLCVQMAAGSGFISGKVKVLLIRLSLSCGNTIN 180
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 116 GLMADRVAICRPPLYSILMSRTVTLKMAAGFAAGLINFMVNTSVSSLSFCDSNVTH 175
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 181 HFECDSPLNLSCTDMSTAELETDEVLATFILLGPLSVTGASYMAITGVMRIPSAAGR 240
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 176 HFECDSPLNLSCTDMSTAELETDEVLATFILLGPLSVTGASYMAITGVMRIPSAAGR 235
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 241 KAFSTCASHLVVITFYAASIFLYARPKALSAFDTNKLVSVLYAVIPLFNPIYCLRNQ 300
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 236 KAFSTCASHLVVITFYAASIFLYARPKALSAFDTNKLVSVLYAVIPLFNPIYCLRNQ 295
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 301 DYKRALRRTL 310
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 296 EYKALANVT 305
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

```

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RX MEDLINE=95394447; PubMed=7665158;
RA Fan W., Liu Y.-C., Parimoo S., Weissman S.M.;
RT "Olfactory receptor-like genes are located in the human major
RT histocompatibility complex."
RL Genomics 27:119-123(1995).
RN [12]
RP SEQUENCE OF 10-312 FROM N.A., AND VARIANTS S-30; V-48 AND A-220.
RX MEDLINE=20341390; PubMed=10880742;
RA Eklund A.C., Belchak M.M., Lapidus K., Raha-Chowdhury R., Ober C.;
RT "Polymorphisms in the HLA-linked olfactory receptor genes in the
RT Hutterites."
RL Hum. Immunol. 61:711-717(2000).
RT -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
RT -1- SUBCELLULAR LOCATION: Integral membrane protein.
RT -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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CC EMBL: L35475; AAB36567.1; -.
DR EMBL: AF211939; AAF98751.1; -.
DR EMBL: AF211940; AAF98752.1; -.
DR EMBL: AF211941; AAF98753.1; -.
DR EMBL: AF211942; AAF98754.1; -.
DR GCRD: GCR_1814; -.
DR MIM: 600578; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family; Olfaction.
FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 23 46 1 (POTENTIAL).
FT DOMAIN 47 55 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 56 77 2 (POTENTIAL).
FT DOMAIN 78 98 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 99 118 3 (POTENTIAL).
FT DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 138 158 4 (POTENTIAL).
FT DOMAIN 159 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 220 5 (POTENTIAL).
FT DOMAIN 221 234 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 235 259 6 (POTENTIAL).
FT DOMAIN 260 270 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 271 290 7 (POTENTIAL).
FT DOMAIN 291 316 CYTOPLASMIC (POTENTIAL).
FT DISULFID 95 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 30 30 F -> S.
FT VARIANT 30 30 F -> S.
FT VARIANT 48 48 A -> V.
FT VARIANT 48 48 A -> V.
FT VARIANT 220 220 T -> A.
FT VARIANT 220 220 /FTID-VAR_010229.
FT CONFLICT 22 22 E -> G (IN REF. 1).
FT CONFLICT 28 28 V -> D (IN REF. 1).
FT CONFLICT 30 30 P -> I (IN REF. 1).
FT CONFLICT 51 51 F -> T (IN REF. 1).
FT CONFLICT 81 81 V -> A (IN REF. 1).
FT CONFLICT 113 114 L -> MK (IN REF. 1).
FT CONFLICT 153 153 E -> G (IN REF. 1).
FT CONFLICT 230 232 KGR -> TAM (IN REF. 1).
FT CONFLICT 267 267 I -> V (IN REF. 1).
FT CONFLICT 287 287 VT -> IK (IN REF. 1).
FT CONFLICT 295 296 F -> L (IN REF. 1).
FT CONFLICT 299 299 F -> L (IN REF. 1).

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FT CONFLICT 307 311 RDSRE -> MGITQ (IN REF. 2).  
SQ SEQUENCE 316 AA; 35410 MW; BE29B672B66A7CE CRC64;

Query Match 39.8%: Score 671; DB 1; Length 316;

Best Local Similarity 46.2%: Pred. No. 6.1e-45;  
Matches 140; Conservative 46; Mismatches 113; Indels 4; Gaps 1;

QY 13 FVLGGPAPAPARLVLFLLSLDVLVLTENMLIIAIRNHPFLHKAHPYFLANMSFLEI 72  
DB 10 FLLGFSEHPLEKTLTLLVVTSTYLLTLVGTLLILSLADPKLHSPYFELSLMSLELD 69  
QY 73 WYVVTIPKMLAGFISGENHGLISFEACMTQLYFELGCTECVLLAVAYRYAIC 132  
DB 70 CFTTSCFQMLVNMGRKT----ISFLDCSVQIFELSLGTTCTCLITLWAFPRYAVC 125  
QY 133 HPLHYPIVYSSRLCYOMAGSMAGSGFISMYKVFELISRLSYCGPNTINHFECVSPLLN 192  
DB 126 QPLHYATIHPLCMQALASVAVMIGLVESVYQTPSTLHLEPCPDROVDCEVPALIRL 185  
QY 193 SCTDMSTAELEDFVALIFILLGLPSVTGASYMATGAVMRIPSAGRHKAFTCSHLTV 252  
DB 186 SCBPTSTNEIOVAVASFLVPLSLVLSGALTMAVLRINSAKGRKAFGTCSSHLTV 245  
QY 253 VILFYASIFITYARPKALSAFDTNKLVSIVYAVIPFNPIYCLRNODYKRALRRLHL 312  
DB 246 VTLFYSYVAVYLOPKNPYAOERGRKFGFLFVAVGTPSLNPLITLNRKEVYRARRLLGK 305  
QY 313 AOD 315  
DB 306 ERD 308

RESULT 13  
O2B2\_HUMAN STANDARD; PRT; 357 AA.

ID O2B2\_HUMAN

AC O9GZK3; O9GZL2; O9Y299;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Olfactory receptor 2B2 (Olfactory receptor 6-1) (OR6-1) (Hs6M1-10).

GN OR2B2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. AND VARIANT ARG-234.

RA Ziegler A., Ehlers A., Forbes S.A., Trowsdale J., Uchanska-Ziegler B.,

RA Volz A., Younger R., Beck S.;

RT "Polymorphic olfactory receptor genes and HLA loci constitute extended

haplotypes.";

RL (in) Kasahara M. (eds.);

RL Major histocompatibility complex-evolution, structure, and function,

RL pp.110-130, Springer-Verlag, Tokyo (2000).

RN [2]

RP SEQUENCE OF 1-310 FROM N.A.

RA Wild A.;

RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

CC - FUNCTION: PUTATIVE ODORANT RECEPTOR.

CC - SUBCELLULAR LOCATION: Integral membrane protein.

CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL; AJ302586; CAC20506.1; -  
DR EMBL; AJ302587; CAC20507.1; -  
DR EMBL; AJ302588; CAC20508.1; -  
DR EMBL; AJ302589; CAC20509.1; -  
DR EMBL; AJ302590; CAC20510.1; -  
DR EMBL; AJ302591; CAC20511.1; -  
DR EMBL; AJ302592; CAC20512.1; -  
DR EMBL; AJ302593; CAC20513.1; -  
DR EMBL; 298744; CAB11427.1; -  
DR Interpro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_RHODPSN.  
DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS00262; G-PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
KW Multigene family; Olfaction; Polymorphism.  
FT DOMAIN 1 25  
FT TRANSMEM 26 49  
FT DOMAIN 50 57  
FT TRANSMEM 58 79  
FT DOMAIN 80 100  
FT TRANSMEM 101 120  
FT DOMAIN 121 139  
FT TRANSMEM 140 158  
FT TRANSMEM 159 195  
FT TRANSMEM 196 219  
FT DOMAIN 220 236  
FT TRANSMEM 237 259  
FT DOMAIN 260 272  
FT TRANSMEM 273 292  
FT DOMAIN 293 357  
FT DISULFID 97 189  
FT CARBOHYD 5 5  
FT VARIANT 234 234  
FT N-LINKED (GLCNAC... ) (POTENTIAL).  
FT O -> R (IN 6M1-10\*42).  
FT /FTID=VAR\_010943.  
SQ SEQUENCE 357 AA; 40412 MW; 53E2F82820BC440A CRC64;  
Query Match 39.7%: Score 670; DB 1; Length 357;  
Best Local Similarity 43.8%: Pred. No. 8.2e-45;  
Matches 130; Conservative 57; Mismatches 106; Indels 4; Gaps 1;  
QY 12 EFLVGGPAPAPARLVLFLLSLDVLVLTENMLIIAIRNHPFLHKAHPYFLANMSFLE 71  
DB 11 EFLVSSDQWLEIPFVYMLFSTYLLFEGNLTIIIVSHVDFKLHPRMYFELSLSLD 70  
QY 72 IWVVTIPKMLAGFISGENHGLISFEACMTQLYFELGCTECVLLAVAYRYAIC 131  
DB 71 LCYTTSTVPQMLVNICNTR---KVISYGCVAOLFELFALGSTECCLLAWCFDFEVAI 126  
QY 132 CHPLHYPIVYSSRLCYOMAGSMAGSGFISMYKVFELISRLSYCGPNTINHFECVSPLLN 191  
DB 127 CRPLHYSTIMHQRICFQDLAASWISGFSNSVLSQSTWTKMKPLCHKEVDFCEVPALK 186  
QY 192 LSCDTMSTAELEDFVALIFILLGLPSVTGASYMATGAVMRIPSAGRHKAFTCSHLTV 251  
DB 187 LSCVDITANAELELFISVLFLLIPVTLILISARIVQAVLRIGSABGRKAFGCGSHLI 246  
QY 252 VILFYASIFITYARPKALSAFDTNKLVSIVYAVIPFNPIYCLRNODYKRALRRL 308  
DB 247 VSLFYSTAISMYLOPPSPSSKDRKMWLSFCGLIAPMLNPLITLNRKEVKEAFKR 303  
RESULT 14  
O2B2\_HUMAN STANDARD; PRT; 312 AA.  
ID O2B2\_HUMAN  
AC O95918;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Olfactory receptor 2H2 (Hs6M1-12).  
GN OR2B2.  
OS Homo sapiens (Human).

Query Match	Best Local Similarity	Score	DB 1	Length	312
Matches 139;	Conservative	45;	Mismatches	110;	Indels 4; Gaps 1;
QY 13	FTLGLGPPAPAPRLVLLFELSLDYLVLVLTENMLITIAIRNHPETLHKPMYFELANNSFLEI	72			
DB 10	FTLLGFGSEHPGLERTLTVVFTSYLLTVLGNLTLLLSALDPLKSPMYFELNSFLDL	69			
QY 73	MYVYVITIRKMLAGFVIGSKENHQLISFECKMQLYFPLGLGCTECVLLAVMAIDRYVAIC	132			
DB 70	CFITSCVPMVLNVMGPKRT---ISFLDCSQVQIFLFLSLGTETCIIITLVAFDRYVAVC	125			
QY 133	HPLHPYIVSVSRSLCQOMAGSWMAGGFGISMYVFLISRSYSCGPMPTINHPFCDVSPPLNTL	192			
DB 126	QPLHATITIHRRCLMQLSAVAMVIGLVSSVYOTPTLHLPFCPDQVDFVCEVALLRL	185			
QY 193	SCDMSFTELDFVLAIFLLGLPVLSTGASYMAITGAVMIRIPISAGRRKAFSTCASHLTV	252			
DB 186	SCEDPSYNEIQVAAVSFVLVPLSLIIVSGAIVMAYLRINSAGRRKAFSTCASHLTV	245			
QY 253	VIFEYASIFLYARPKALSADFTNKLVSVAIVYPLFNPIITYCLRNODVYKALRRTL	310			
DB 246	VTLFSSYIAVYLPQKNPYAQDRGKFFGLFAYAVGTPPSINPLIYTLRNKEVTRAFRRLL	303			

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02B6_HUMAN STANDARD: PRT: 313 AA.
AC P58173; Q9H5B0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 2b6 (Hs6M1-32) (Olfactory receptor 6-31) (OR6-31).
GN OR2B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb.sib.ch).
CC -----
CC EMBL: AL133267; CAC14158.1; -.
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSNM 26 49 1 POTENTIAL.
FT TRANSNM 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSNM 58 79 2 POTENTIAL.
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSNM 101 120 3 POTENTIAL.
FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
FT TRANSNM 140 158 4 POTENTIAL.
FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
FT TRANSNM 196 219 5 POTENTIAL.
FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
FT TRANSNM 237 259 6 POTENTIAL.
FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
FT TRANSNM 273 292 7 POTENTIAL.
FT DOMAIN 293 313 CYTOPLASMIC (POTENTIAL).
FT DISULFD 97 189 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 313 AA; 35414 MW; 71D459541ACF5301 CRC64;

Query Match 39.5%; Score 667; DB 1; Length 313;
Best Local Similarity 44.1%; Pred. NO. 1.2e-44;
Matches 132; Conservative 54; Mismatches 109; Indels 4; Gaps 1;

0Y 10 VSEFPLGFPAPAPRLVLLFFSLDLYLVLTENMLITIAIRNPILAKPRYFFLAMSKF 69
Db 9 IQEFLILGSDRPWLEPFLVAVFLISVTYTFNGMLITILVSRDTRKLTHTPEFLTNLSL 68
0Y LEIWWVATITIKMLAGFSGKENHGQLSFSPACMTOLYFFGLGCTCECVLLAVNAYDRV 129
Db 69 LDLCYTTCTVQMLVNLCSIR---KVIYSGCAVQLFTFLALDATEYLLAVMSFDFEV 124
0Y AICPILAHPIVYSRSLQVOMAGSMAGFGFSGISAMKVFILSRSLSCGPNITNHFPCDVSPL 189
Db 125 AICRPLAHSVIMHQRCLQGLAASAMVYGFNSVWLSTLTIDPLPCDPRVIDHFLCEVPAL 184
0Y LNLSCDMSVTAELTDEVLAIFILLGPIASVTGASVYMAITGAVMRIPSAAGRKAFTSCASH 249

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Db 185 LKISCVEFTANESELPVSELPFLIPFLILISYAFIVRAVLRIOSAEGRKAFGTGSH 244  
QY 250 LTVVITFEYASTIFIVARPKALSAFDINKLVSVLYANIVPLFNPIIYCLRNQDYKRALRR 308  
Db 245 LIVVSLFYSTAVSVYLQPPSPSSKDGKMSLEYGIIAPMLNPLIYTLRNKEVKEGFKR 303

Search completed: May 22, 2002, 15:43:55  
Job time: 409 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 22, 2002, 15:31:37 ; Search time 17.62 Seconds  
(without alignments)  
1783.270 Million cell updates/sec

Title: US-09-771-209-76

Perfect score: 1687

Sequence: 1 MERRNHSGRVSEFVLLGFPD.....RTLHLAODQEAANTNKGSKIG 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1680	99.6	327	2 F23701	olfactory receptor
2	788	46.7	311	2 C23701	olfactory receptor
3	751	44.5	222	2 B40745	odorant receptor (
4	666	39.5	315	2 JC5836	olfactory receptor
5	657.5	39.0	318	2 JC5202	chemoreceptor T864
6	656.5	38.9	313	2 B23701	olfactory receptor
7	650	38.5	316	2 A57069	olfactory receptor
8	644	38.2	312	2 A46247	olfactory receptor
9	642	38.1	305	2 S29711	olfactory factor O
10	636.5	37.7	313	2 S20571	olfactory receptor
11	636	37.7	320	2 S20573	olfactory receptor
12	635	37.6	314	2 A37286	olfactory receptor
13	625	37.0	312	2 I23701	olfactory receptor
14	623.5	37.0	309	1 S51356	olfactory receptor
15	623	36.9	311	2 JC5200	olfactory receptor
16	623	36.9	311	2 JC5202	chemoreceptor T833
17	621	36.8	304	2 S29709	olfactory receptor
18	616.5	36.5	314	2 H23701	olfactory receptor
19	616.5	36.5	319	2 JC5624	olfactory receptor
20	613.5	36.4	312	2 A48413	probable olfactory
21	608.5	36.1	307	2 S29710	olfactory receptor
22	607	36.0	315	2 JC4658	olfactory receptor
23	606.5	36.0	333	2 A23701	olfactory receptor
24	605.5	35.9	314	2 S29707	olfactory receptor
25	605	35.9	317	2 D23701	olfactory receptor
26	600	35.6	312	2 S29708	olfactory receptor
27	587	34.8	310	2 E23701	olfactory receptor
28	573	34.0	315	2 JC5201	chemoreceptor T856
29	570	33.8	312	2 G23701	olfactory receptor

30	524	31.1	312	2 A46750	olfactory receptor
31	500.5	29.7	264	2 PC4369	olfactory receptor
32	467	27.7	222	2 D40745	odorant receptor (
33	451	26.7	234	2 S29000	G protein-coupled
34	449	26.6	216	2 I38480	olfactory receptor
35	445	26.4	232	2 S29001	G protein-coupled
36	440	26.1	216	2 I38481	olfactory receptor
37	438.5	26.0	328	2 G45774	odorant receptor 2
38	431	25.5	216	2 I38479	olfactory receptor
39	431	25.5	234	2 S28998	G protein-coupled
40	430	25.5	216	2 I38478	olfactory receptor
41	426.5	25.3	225	2 I38478	olfactory receptor
42	424	25.1	216	2 I38470	olfactory receptor
43	423	25.1	216	2 I38476	olfactory receptor
44	421.5	25.0	215	2 I38473	olfactory receptor
45	410	24.3	222	2 C40745	odorant receptor (

ALIGNMENTS

RESULT 1  
F23701  
olfactory receptor I7 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 26-Aug-1999  
C:Accession: F23701  
R:Buck, L.; Axel, R.  
Cell 65, 175-187, 1991  
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for  
A:Reference number: A23701; MUID:91191556  
A:Accession: F23701  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-327 <BUC>  
A:Cross-references: GB:M64386; NID:g205833; PIDN:AAA41749.1; PID:g205834  
C:Superfamily: olfactory receptor OR14  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 99.6%; Score 1680; DB 2; Length 327;  
Best Local Similarity 99.7%; Pred. No. 1.2e-140;  
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MERRNHSGRVSEFVLLGFPAPAPRLVLLPFLSLDYVLTPENNMLITAIRNHPPLKPM	60
DB	1	MERRNHSGRVSEFVLLGFPAPAPRLVLLPFLSLDYVLTPENNMLITAIRNHPPLKPM	60
QY	61	YFELANMSFLEIWTYVTVTIIPKMLAGFISKENHGOLISFEACMTOLYFELGIGCTECVLL	120
DB	61	YFELANMSFLEIWTYVTVTIIPKMLAGFISKENHGOLISFEACMTOLYFELGIGCTECVLL	120
QY	121	AVMAIDRYVAICHPLHAYIYVSSRLCYOMAGSNAGGGSISWVKFKLISRLSYCGPNTIN	180
DB	121	AVMAIDRYVAICHPLHAYIYVSSRLCYOMAGSNAGGGSISWVKFKLISRLSYCGPNTIN	180
QY	181	HFPCVSPFLNLSCTDMSTAEITDFVLAIFITLGLPSTGASYMTAGVMMIPSAAGR	240
DB	181	HFPCVSPFLNLSCTDMSTAEITDFVLAIFITLGLPSTGASYMTAGVMMIPSAAGR	240
QY	241	KAFTCSASHLVVLIIFVAASIFIVARPKALSAFTNKLVSVLVAVIVLPFNIIYCLRNQ	300
DB	241	KAFTCSASHLVVLIIFVAASIFIVARPKALSAFTNKLVSVLVAVIVLPFNIIYCLRNQ	300
QY	301	DVKRALRRTLHLAODQEAANTNKGSKIG	327
DB	301	DVKRALRRTLHLAODQEAANTNKGSKIG	327

RESULT 2  
C23701  
olfactory receptor F6 - rat  
C:Species: Rattus norvegicus (Norway rat)



A:Reference number: JC5200; MUID:97080538  
A:Accession: JC5202  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-318 <TH01>  
A:Cross-references: GB:U0949; NID:g1256392; PIDN:AAC52911.1; PID:g1256393  
A:Accession: PC4304  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 145-153; 245-253 <TH02>  
A:Experimental source: taste bud  
C:Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction  
C:Genetics:  
A:Gene: tb641  
C:Superfamily: olfactory receptor OR14  
C:Keywords: olfaction; taste bud; transmembrane protein  
E:30-53/Domain: transmembrane #status predicted <TM1>  
E:63-84/Domain: transmembrane #status predicted <TM2>  
E:106-125/Domain: transmembrane #status predicted <TM3>  
E:145-169/Domain: transmembrane #status predicted <TM4>  
E:202-224/Domain: transmembrane #status predicted <TM5>  
E:243-265/Domain: transmembrane #status predicted <TM6>  
E:276-296/Domain: transmembrane #status predicted <TM7>

Query Match	39.0%	Score 657.5	DB 2	Length 318
Best Local Similarity	42.3%	Pred. No. 1.8e-50		
Matches 135; Conservative	56;	Mismatches 101;	Indels 27;	Gaps 6;

[illegible]

RESULT 6  
B23701  
Olfactory receptor F5 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 04-Sep-1998  
C:Accession: B23701  
R:Buck, L.; Axel, R.  
Cell 65, 175-187, 1991  
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od  
A:Reference number: A23701; MUID:91191556  
A:Accession: B23701  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-313 <BUC>  
A:Cross-references: GB:M64377  
C:Superfamily: Olfactory receptor OR14  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	38.98;	Score 656.5;	DB 2;	Length 313;
Best Local Similarity	44.18;	Pred. No. 2.2e-50;		
Matches 137;	Conservative 50;	Mismatches 117;	Indels 7;	Gaps

[illegible]

RESULT 7  
A57069  
Olfactory receptor FAT11 - human  
C:Species: Homo sapiens (man)  
C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 26-Aug-1999  
C:Accession: A57069  
R:Pan, W.; Liu, Y. C.; Parmico, S.; Weissman, S.M.  
Genomics 27, 119-123, 1995  
A:Title: Olfactory receptor-1like genes are located in the human major histocompabil  
A:Reference number: A57069; MUID:95394447  
A:Accession: A57069  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-316 <FAN>  
A:Cross-references: GB:J35475; NID:g1041044; PIDN:AAB36567.1; PID:G601919  
C:Genetics:  
A:Gene: GDB:FAT11; OLF2  
A:Cross-references: GDB:132349; OMIM:600578  
A:Map position: 6p21.3-6p21.3  
C:Superfamily: olfactory receptor OR14

Query Match	38.5%;	Score 650;	DB 2;	Length 316;
Best Local Similarity	45.2%;	Pred. NO. 8.2e-50;		
Matches 137;	Conservative 48;	Mismatches 114;	Indels 4;	Gaps 1;

```

OY      FVGCPAPAPLRYLVEFLSLDDVLAIVTEMLIIIRNHPHAKHMYEFANMSLEI  72
      1  : : : : : 1  : : : : : 1  : : : : : 1  : : : : :
Db      FLFLGFSHRLQGLTEVDVITYSLTLVYCNLTLLIISALDTRKHSNMYEFLSNLSLDL  69
      10  : : : : : 10  : : : : : 10  : : : : : 10  : : : : :
OY      WYVTVTLPKMLAGTSGKENHGOLISEACTOLTFPLGLGCEVCVLLAAMAYDRYATC  132
      73  : : : : : 73  : : : : : 73  : : : : : 73  : : : : :
Db      CFTTSCVPQMLANLMGRKPT---ISFLDSSVQIFELSGTECEILMKMAEDRYAVAC  125
      70  : : : : : 70  : : : : : 70  : : : : : 70  : : : : :
OY      HPILHYPIVYSRLCLVQMAAGSMAGGFGISMYKVELIRLSYCGPNTIHFECVSPYLNT  192
      133  : : : : : 133  : : : : : 133  : : : : : 133  : : : : :
Db      QPLHAYATIHPRLCMOLASVAMVIGLVGSVYQFSTHLRFCCPRQVDDVCEVPALIRL  185
      126  : : : : : 126  : : : : : 126  : : : : : 126  : : : : :
OY      SCTQMSMAELTDFLALIFILLGRPLSYGASVMAITGVAVMIPRSAGCNHKAFCASHLTV  252
      193  : : : : : 193  : : : : : 193  : : : : : 193  : : : : :
Db      SCEPTSTNEIYAVASVFIIVPLSLTLLSVYSGAITMAVLVINSRTAMRKKAFGCTSHLY  245
      186  : : : : : 186  : : : : : 186  : : : : : 186  : : : : :
OY      VIIFEASIFLYAPKALSAFDNKLVSILYAVIVLPENFIYCLRNQDVKRALRRTLHL  312
      253  : : : : : 253  : : : : : 253  : : : : : 253  : : : : :

```

Db 246 VTLFYSSVIAVYIQPKNPYAQGRKGFGLFYANGTSPSLNPLVLTNRKKEIKRALRLLG 305  
QY 313 AOD 315  
Db 306 ERD 308

RESULT 8  
A46247  
olfactory receptor OR3 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 26-Aug-1999  
C:Accession: A46247  
R:Neef, P.; Hermans-Borgmeyer, I.; Artieres-Pin, H.; Beasley, L.; Dionne, V.E.; Heinemann  
Proc. Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992  
A:Title: Spatial pattern of receptor expression in the olfactory epithelium.  
A:Reference number: A46247; MUID:93028384  
A:Accession: A46247  
A:Status: Preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-312 <NEF>  
A:Cross-references: GB:M84005; NID:g200153; PIDN:AAA39862.1; PID:g200154  
A:Note: sequence extracted from NCBI backbone (NCBIP:115362)  
C:Superfamily: olfactory receptor OR14

Query Match 38.2%; Score 644; DB 2; Length 312;  
Best Local Similarity 43.0%; Pred. No. 2,7e-49;  
Matches 128; Conservative 55; Mismatches 111; Indels 4; Gaps 1;

QY 13 FVLGGPAPAPRVLLFSLSDIVLVLTENMLIIRNHPILHKKMPYFFLANMSFLEI 72  
Db 12 FILMGVSDHPLHIIFFAVILASVLTGLVNLIIILSRDARLHMPYFFLSMSLIDL 71  
QY 73 WYVTVTIPKMLAGFISKENHGLISPEACMTQLYFLGCTECVLLAVMAYDRYVAIC 132  
Db 72 AFTTSSVPQMLKMLMGPDRTK----ISYGCCTQLYVFLMGATECILLVMAEDRYAVC 127  
QY 133 HPLHYPIVYSSRLCVQMAAGSMAGGFGISMKVYKLLISRLSYCGPNTINHFCDVSPLLNT 192  
Db 128 RPLHYMTVMNPRILCMGLAISMLGSLGNSVYIQSTFTQLPFCGHRKVDNLCFEPAMIKL 187  
QY 193 SCIDMSTAEITDVLAFILILGPLSVTGASYMATGAVMRIPSAAGHKKAFSTCASHLTV 252  
Db 188 ACGDSTLNEVLNGVCTFTVPVSVLYVSYCTLAQVAMKIRSEGRKKAFCVSHLVV 247  
QY 253 VILFYASIFIVARPKALSAFDTNKLVSVYAVIVLPFNPIIYCLRNQDVKRALRLTV 310  
Db 248 VLFYGSATIGYLLPAKSSNQSGKFIISLYSVTPRVNPLIITLRKKEYGKALGRLL 305

RESULT 9  
S29711  
olfactory factor OR37 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 04-Sep-1998  
C:Accession: S29711  
R:Ramung, K.; Krieger, J.; Strotmann, J.; Boehkoff, I.; Kubick, S.; Baumstark, C.; Breech  
Nature 361, 353-356, 1993  
A:Title: Cloning and expression of odorant receptors.  
A:Reference number: S29707; MUID:93149273  
A:Accession: S29711  
A:Molecule type: mRNA  
A:Residues: 1-305 <RAM>  
C:Superfamily: olfactory receptor OR14

Query Match 38.1%; Score 642; DB 2; Length 305;  
Best Local Similarity 43.9%; Pred. No. 4e-49;  
Matches 133; Conservative 57; Mismatches 103; Indels 10; Gaps 3;

QY 14 VILGGPAPAPRVLLFSLSDIVLVLTENMLIIRNHPILHKKMPYFFLANMSFLEIW 73  
Db 13 VILGGPAPAPRVLLFSLSDIVLVLTENMLIIRNHPILHKKMPYFFLANMSFLEIW 73

Db 1 LLLGLSGPKTEILFVIVLVYVLIHTGNGVLIITASIPDSHLTPMYFFLGNI-SFLDIC 60  
QY 74 YVTVTIKMLAGFISKENHGLISPEACMTQLYFLGCTECVLLAVMAYDRYVAIC 133  
Db 61 YTTSSVPSTVLSLKKRN----ISFGCTVQMGVGFAMSGSTECILLGNMAFDRYVAICN 116  
QY 134 PLHYPIVYSSRLCVQMAAGSMAGGFGISMKVYKLLISRLSYCGPNTINHFCDVSPLLNLS 193  
Db 117 PLRYVIMSKREKVVYMASASWFGSGINSVQTSILAMRLPFCGNVNIHFCEVALVTLKA 176  
QY 194 CTDKSTAEITDVLAFILILGPLSVTGASYMATGAVMRIPSAAGHKKAFSTCASHLTV 253  
Db 177 CADISLNIWTVISNMALVPLPLIFFSTVLIITLRKMSASGRKRAFSTCASHLTV 236  
QY 254 IIFYASIFIVARPKA--LSAFD----TNKLVSVYAVIVLPFNPIIYCLRNQDVKRALR 307  
Db 237 VIEGTIFSMYAKRKQDLGKDKFQTSIDKILISLFYGVYPMPLPIIYSLRNKQVKAAYK 296  
QY 308 RTL 310  
Db 297 YIL 299

RESULT 10  
S20571  
olfactory receptor - dog  
C:Species: Canis lupus familiaris (dog)  
C:Date: 22-Nov-1993 #sequence\_revision 01-Dec-1995 #text\_change 26-Aug-1999  
C:Accession: S20571  
R:Parmentier, M.; Libert, F.; Schirrans, S.; Schlifmann, S.; Lefort, A.; Eggerickx, D  
Nature 355, 453-455, 1992  
A:Title: Expression of members of the putative olfactory receptor gene family in mamm  
A:Reference number: S20571; MUID:92131132  
A:Accession: S20571  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-313 <PAR>  
A:Cross-references: EMBL:X64996; NID:g890; PIDN:CAA46129.1; PID:g891  
C:Superfamily: olfactory receptor OR14  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 37.7%; Score 636.5; DB 2; Length 313;  
Best Local Similarity 43.2%; Pred. No. 1.3e-48;  
Matches 130; Conservative 55; Mismatches 111; Indels 5; Gaps 2;

QY 10 VSEFVLGPAPAPRVLLFSLSDIVLVLTENMLIIRNHPILHKKMPYFFLANMSF 69  
Db 9 VSEFVLGLPIDDPQKRLFYALFLAMVYTIILGNLITVLQDLSHLHTPMYFLSMUSF 68  
QY 70 LEIWTYVTIPKMLAGFISKENHGLISPEACMTQLYFLGCTECVLLAVMAYDRYV 129  
Db 69 SDLCFSSVTMPKLLQ---NMQSQVPSIPYAGCLTQMYFFLFEGDLSPLLVAMAYDRYV 124  
QY 130 ALCHPLHYPIVYSSRLCVQMAAGSMAGGFGISMKVYKLLISRLSYCGPNTINHFCDVSP 189  
Db 125 ALCEPLHYTTIMSPKLCFSLVLSWVLTMFHAVLHTLMARLCECA--NTLPHFCDMSAL 183  
QY 190 LNIQCTMSTAEITDVLAFILILGPLSVTGASYMATGAVMRIPSAAGHKKAFSTCAS 249  
Db 184 LKLAQSTQYNELVIFMGILLIYIPFLIITTSARLVSSILKVPASIGCKVFTCGSH 243  
QY 250 LTVVILFYASIFIVARPKALSAFDTNKLVSVYAVIVLPFNPIIYCLRNQDVKRALRLTV 309  
Db 244 LSVVSLFYGVIGYLCPSANNSTVKKETIMAMVYTVTPPLNPIIYSLRNKDKMGALRRV 303  
QY 310 L 310  
Db 304 I 304

RESULT 11  
S20573



```
QY 10 USEFVLLGFAPAPAPLRLVLEFLSLDYVLVTENMLIIAIRNHPTLHKPMYFFLANMSF 69
    :|:|:| | : : : | | : : |::| | | | | | | | | | | |
Db 9 ISQFLLEFLPISEHQHYALFLSMYLTIVLGNLIIILIHDSHLHPMYLPLSNLSF 68
```

RESULT 14  
S51356  
olfactory receptor - rat



GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: May 22, 2002, 15:30:55 ; Search time 13.05 seconds  
(without alignments)  
612.044 Million cell updates/sec

Title: US-09-771-209-76

Perfect score: 1687

Sequence: 1 MERRHNSGRSEFVLLGPPA.....FTLHLADQDEANTNGSKIG 327

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1382.5	82.0	286	1	US-08-118-270-65
2	1382.5	82.0	286	5	PCT-US93-08528-65
3	705	41.8	277	1	US-08-118-270-62
4	705	41.8	277	5	PCT-US93-08528-62
5	668	39.6	321	4	US-08-748-506-18
6	668	39.6	321	4	US-08-748-506-10
7	660	39.1	321	4	US-08-748-506-20
8	658	39.0	321	4	US-08-748-506-11
9	658	39.0	321	4	US-08-748-506-12
10	654	38.8	321	4	US-08-748-506-19
11	653	38.7	321	4	US-08-748-506-13
12	633.5	37.6	327	4	US-08-748-506-24
13	623.5	37.0	327	4	US-08-748-506-14
14	623	36.9	314	3	US-08-988-876-7
15	616	36.5	327	4	US-08-748-506-22
16	616	36.5	327	4	US-08-748-506-23
17	614.5	36.4	309	3	US-08-988-876-5
18	607	36.0	284	1	US-08-118-270-61
19	607	36.0	284	5	PCT-US93-08528-61
20	606.5	36.0	333	3	US-08-988-876-6
21	599	35.5	316	2	US-08-827-291A-2
22	575.5	34.1	296	2	US-08-467-948A-2
23	575.5	34.1	296	3	US-08-467-947A-2
24	524.5	31.1	293	1	US-08-118-270-60
25	524.5	31.1	293	5	PCT-US93-08528-60
26	517.5	30.7	274	1	US-08-118-270-69
27	517.5	30.7	274	5	PCT-US93-08528-69

28	514	30.5	247	1	US-08-465-980-3	Sequence 3, App1
29	514	30.5	247	2	US-09-053-303-3	Sequence 3, App1
30	514	30.5	247	5	PCT-US93-07093-3	Sequence 3, App1
31	513.5	30.4	284	1	US-08-118-270-67	Sequence 67, App1
32	513.5	30.4	284	5	PCT-US93-08528-67	Sequence 67, App1
33	506	30.0	100	4	US-09-085-371-6	Sequence 68, App1
34	498.5	29.5	277	5	PCT-US93-08528-68	Sequence 68, App1
35	498.5	29.5	277	1	US-08-118-270-68	Sequence 68, App1
36	496	29.4	273	1	PCT-US93-08528-63	Sequence 63, App1
37	496	29.4	273	5	PCT-US93-08528-63	Sequence 63, App1
38	467	27.7	222	2	US-08-467-948A-27	Sequence 27, App1
39	467	27.7	222	3	US-08-467-947A-27	Sequence 27, App1
40	456	27.0	275	1	US-08-118-270-66	Sequence 66, App1
41	456	27.0	275	5	PCT-US93-08528-66	Sequence 66, App1
42	437	25.9	269	1	US-08-118-270-64	Sequence 64, App1
43	437	25.9	269	5	PCT-US93-08528-64	Sequence 64, App1
44	407	24.1	320	4	US-09-439-313-527	Sequence 527, App1
45	396	23.5	320	1	US-08-465-980-2	Sequence 2, App1

## ALIGNMENTS

RESULT 1  
US-08-118-270-65  
: Sequence 65, Application US/08118270  
: Patent No. 5508384  
: GENERAL INFORMATION:  
: APPLICANT: Murphy, Randall B.  
: APPLICANT: Schuster, David I.  
: TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
: TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
: NUMBER OF SEQUENCES: 348  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: BROWDY AND NEIMARK  
: STREET: 419 Seventh Street, N.W., Suite 300  
: CITY: Washington  
: STATE: D.C.  
: COUNTRY: USA  
: ZIP: 20004  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/118,270  
: FILING DATE: 09-SEP-1993  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/943,236  
: FILING DATE: 10-SEP-1992  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Townsend, Kevin G.  
: REGISTRATION NUMBER: 34,033  
: REFERENCE/DOCKET NUMBER: MURPHY-2A  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 202-628-5197  
: TELEFAX: 202-737-3528  
: TELEX: 248633  
: INFORMATION FOR SEQ ID NO: 65:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 286 amino acids  
: TYPE: amino acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: peptide  
: US-08-118-270-65

Query Match 82.0% Score 1382.5; DB 1; Length 286;  
Best Local Similarly 91.7% Pred. No. 3.5e-116;  
Matches 276; Conservative 4; Mismatches 6; Indels 15; Gaps 4;

OY 27 LFFLSLDIVLVLTENMLIIIRNHPPLHKMYFFLANMSFLEIWTYVTITPKMLAGF 86  
|||||  
Db 1 LFFFLSLXYVLVTENMLIIIRNHPPLHKMYFFL-----FLEIWTYVTITPKLM-GF 55  
OY 87 IGSKENHGOLISFEACMTQLYFFLGCTECVLLAWAANDRYVAICHPPLHYPIVSSRLC 146  
|||||  
Db 56 IGSKENHGOLISFEACMTQLYFFLGCTECVLLAWAANDRYVAICHPPLHYPIVSSRLC 115  
OY 147 VOMASMGAGFGISVWKVFLISRLSYCGPNTINHFECVSPPLNLSCTDMSTAELTDFV 206  
116 V---LGSWAGFGISVWKVFLISRLSYCGPNTINHFECVSPPLNLSCTDMSTAELTDFV 172  
OY 207 LAIFILLGPLSTGASTYMAITGAVMRIPSAAGRHKAFSTCASHLTVIIFVAAISFIYAR 266  
173 IAFILLGPLSTGASTYMAITGAVMRIPSAAGRHKAFSTCASHLTVIIFVAAISFIYAR 225  
OY 267 PKALSAFDNKLVSIVYAVIVPLFNPIIYCLRQDVKRALRRTLHLAODEANTNGSKI 326  
Db 226 PKALSAFDNKLVSIVYAVIVPLFNPIIYCLRQDVKRALRRTLHLAODEANTNGSKI 285  
OY 327 G 327  
1  
Db 286 G 286

RESULT 2  
PCT-US93-08528-65  
; Sequence 65, Application PC/TUS9308528  
; GENERAL INFORMATION:  
; APPLICANT: New York University  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08528  
; FILING DATE: 09-SEP-1993  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,236  
; FILING DATE: 10-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 286 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; PCT-US93-08528-65

Query Match 82.0%; Score 1382.5; DB 5; Length 286;  
Best Local Similarity 91.7%; Pred. No. 3.5e-116;  
Matches 276; Conservative 4; Mismatches 6; Indels 15; Gaps 4;

OY 27 LFFLSLDIVLVLTENMLIIIRNHPPLHKMYFFLANMSFLEIWTYVTITPKMLAGF 86  
|||||  
Db 1 LFFFLSLXYVLVTENMLIIIRNHPPLHKMYFFL-----FLEIWTYVTITPKLM-GF 55  
OY 87 IGSKENHGOLISFEACMTQLYFFLGCTECVLLAWAANDRYVAICHPPLHYPIVSSRLC 146  
|||||  
Db 56 IGSKENHGOLISFEACMTQLYFFLGCTECVLLAWAANDRYVAICHPPLHYPIVSSRLC 115  
OY 147 VOMASMGAGFGISVWKVFLISRLSYCGPNTINHFECVSPPLNLSCTDMSTAELTDFV 206  
116 V---LGSWAGFGISVWKVFLISRLSYCGPNTINHFECVSPPLNLSCTDMSTAELTDFV 172  
OY 207 LAIFILLGPLSTGASTYMAITGAVMRIPSAAGRHKAFSTCASHLTVIIFVAAISFIYAR 266  
173 IAFILLGPLSTGASTYMAITGAVMRIPSAAGRHKAFSTCASHLTVIIFVAAISFIYAR 225  
OY 267 PKALSAFDNKLVSIVYAVIVPLFNPIIYCLRQDVKRALRRTLHLAODEANTNGSKI 326  
Db 226 PKALSAFDNKLVSIVYAVIVPLFNPIIYCLRQDVKRALRRTLHLAODEANTNGSKI 285  
OY 327 G 327  
1  
Db 286 G 286

RESULT 3  
US-08-118-270-62  
; Sequence 62, Application US/08118270  
; Patent No. 5508384  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Randall B.  
; APPLICANT: Schuster, David I.  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/118,270  
; FILING DATE: 09-SEP-1993  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,236  
; FILING DATE: 10-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: MURPHY-2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 277 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-118-270-62

Query Match 41.8%; Score 705; DB 1; Length 277;  
Best Local Similarity 49.7%; Pred. No. 1.2e-55;

Query Match	41.8%	Score 705;	DB 5;	Length 277;
Best Local Similarity	49.7%	Pred. No. 1.2e-55;		
Matches 142;	Conservative 41;	Mismatches 89;	Indels 14;	Gaps 4.
OY	27	LIFFLSLDDYVVLVENNMILIAINHPFL--HKWYFFFLANMSFLFLEIYVYVTVIPKMLA	-84	

QY	27	FLFSLDLDVYLTENMLIIIIIRNPPTLKPAYFLPANNFSLEIYVYVTPITPLAGE	86
		: : :     : : :     : : :     : : :     : : :     : : :	
Db	32	FLIILIMFLVSLTGNLIYLAICTSPSLHTPRYFLANLSILEICTGCVSPKMLQSL	91
QY	87	IGSENHGQLISFLACMTQLTFLFLGCTCTCYVLLAWAYDRYVAICHPHPIVYSRILC	146
		: : :     : : :     : : :     : : :     : : :     : : :     : : :	
Db	92	V---SEARLETSRSGCATQIMFFAFGLTTECCLLAANAIFDCMAICTSPHLATRMSREVC	147

```

0Y 147 VQMAAGSAGGCGISMWKVELLSRLSGCPNTINHFCDVSPPLNLSCTDMSTAEITDFV 206
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 148 AHAIAVSMGCGIVSLGGQNTFSLNFCGCEIDHFCDPLPLALACGDTSONEATIV 207
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
0Y 207 LAIFLLGPGYSTGASVMAITGAVMRIPSPASMRKKAFTSCASHLVIIIFYAASIFIYAR 266
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 208 VAVLCSIFPELLIIVSYKILIAVLIMPSPBCKRKLKSLSCSSHLIVLTFYSCACTIYR 267
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
0Y 267 PKALSAFDTNKLVSILYANIVLEPNPIITCLNODYKALRLRLHL 312
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 268 PKSSHSPGMDKFLAFTYVTVMLENDPIIYSLRNKEVKALRLRLGL 313
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

RESULT 6
US-08-748-506-10
; Sequence 10, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-748-506-10

Query Match 39.5%; Score 666; DB 4; Length 321;
Best Local Similarity 47.6%; Pred. No. 4.2e-52;
Matches 136; Conservative 46; Mismatches 100; Indels 4; Gaps 1.

```

Dd	208	PALSAFDTNKLVSYLVAIVPLFNEDPIYCLRNQDVKRLRRTLHL	312
Oy	267	PALSAFDTNKLVSYLVAIVPLFNEDPIYCLRNQDVKRLRRTLHL	312
Dd	268	PKSSHSPGMDKFLAFYTVVTSMLNPDIYSLRNKKEVKALRRTLGL	313
		RESULT 7	
		US-08-748-506-20	
		: Sequence 20, Application us/08748506	
		: Patent No. 6159707	
		: GENERAL INFORMATION:	
		: APPLICANT: Ronnett et al.	
		: TITLE OF INVENTION: NOVEL SPERM RECEPTORS	
		: NUMBER OF SEQUENCES: 31	
		: CORRESPONDENCE ADDRESS:	
		: ADDRESSEE: Leydig, Voit & Mayer, Ltd.	
		: STREET: Two Prudential Plaza, Suite 4900	
		: CITY: Chicago	
		: STATE: IL	
		: COUNTRY: US	
		: ZIP: 60601-6780	
		: COMPUTER READABLE FORM:	
		: MEDIUM TYPE: Floppy disk	
		: OPERATING SYSTEM: IBM PC compatible	
		: SOFTWARE: Patentin Release #1.0, Version #1.25	
		: CURRENT APPLICATION DATA:	
		: APPLICATION NUMBER: US/08/748,506	
		: FILING DATE: 08-NOV-1996	
		: CLASSIFICATION: 435	
		: PRIOR APPLICATION DATA:	
		: APPLICATION NUMBER: US 60/033,751	
		: FILING DATE: 09-NOV-1995	
		: CLASSIFICATION: 435	
		: ATTORNEY/AGENT INFORMATION:	
		: REFERENCE/DOCKET NUMBER: 79490	
		: TELECOMMUNICATION INFORMATION:	
		: TELEPHONE: 312-616-5700	
		: TELEFAX: 312-616-5600	
		: INFORMATION FOR SEQ ID NO: 20:	
		: SEQUENCE CHARACTERISTICS:	
		: LENGTH: 321 amino acids	
		: TYPE: amino acid	
		: TOPOLOGY: unknown	
		: MOLECULE TYPE: protein	
		: US-08-748-506-20	
		Query Match 39.1%; Score 660; DB 4; Length 321;	
		Best Local Similarity 47.6%; Pred. No. 1.4e-51;	
		Matches 136; Conservative 47; Mismatches 99; Indels 4; Gaps 2	
Oy	27	LLEFLSLDYVLVNLENMLLIAIRNHPIIHKPMYFELANMSFLEIMWYTAVTIPKMLAGF	86
Dd	32	LFTTLILMLEVLSTGNLIIAICTSLSLHPMFELLNLSDLLEIGTCVIPKMGSL	91
Oy	87	IGSKENHGQLISFEACMTQLYFFELGGCECYLLAVMAAYDRVVALCHPLHYDVVISRRLC	146
Dd	92	V--SEARG--ISMEECASDMFFEIFFEGITTECCOLLAMAEADRKMALCPSLPHYATRMRSRGVC	147
Oy	147	VQMAAGSMWNGFGISMVKVELLSRLSYCGPNTINHFFCDVDSPFLNLSCTDMSJAETLDFEV	206
Dd	148	AYLAIYVMWGCVIGLGQTNFISSLNFCGPCEIDHFCDLPPLLALACGDTSQNEAIFV	207
Oy	207	LAIFILLGPLASTGSYMAITGAVKRKIPSAGRHKAFTSCASHLTVAIVIIFYAAISFIYAR	266
Dd	208	AAVLICFPSPFLLIISYYAHIIAVALVMPSEPGRHRALSCTSSHLLVTLFYGSTSATYLR	267
Oy	267	KALSAFDTKLVSVLVAIVPLFNPIYCLRNQDVKRLRRTLHL	312
Dd	268	SXSHSPGVDKLLAFYTSVTSMLNPDIYSLRNKKEVKALRRTLGL	313



```

; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-748-506-19

```

```

Query Match      38.8%; Score 654; DB 4; Length 321;
Best Local Similarity 46.8%; Pred. No. 5e-51;
Matches 137; Conservative 42; Mismatches 110; Indels 4; Gaps 1;

```

```

QY 27 LLEFLSLDYLVLVTENMLIIIRNHPFLHAKPMYFFLANMSFLEIYYVTITPKMLAGF 86
   ||| ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 32 LLEFLTLMLFVLSTGNALALACTSPSLHTPMYFFLANLSLEIGYCSVIPKMLQSL 91
   ||| ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 87 IGSKENHGOLISFEACMTOLYFFLGCTECVLLAVMADRYVAIGHPLHYPIVSRIC 146
   : ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 92 V-----SEARISREGCATQMEFFTFGITECCLLAAMAEFRMGICSPHYATRMSREVC 147
   : ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 147 VQMAAGSMAGFGISWVKYFELISRLSYCGPNTINHFCDVSPLLNLCSTDMSTAEITDFV 206
   : ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 148 AHLAIYSWMGCIYGLQGTNNIISLNFCCGEIDHFFCDLPPLALACDTSQNEAIEFV 207
   : ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 207 LAIFILLGPLSVGASYMAITGAVMRIPSAAGRHKAFTSCASHLYVIIIFYASITFYAR 266
   ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 208 AALICISPELVLYSYVRLVAVLWVPSEGRHKALSTCSSHLVLTLYFGSVSTFYLR 267
   ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 267 PKALSAFDNTKLIVSYAVIVPLFNPIIYCLRNODVKRALRRLTLHAODQEAN 319
   ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 268 PKSSHSPGMDKLALFTYATVTSMLNPIIYSLRNKDYKALRLTLDLKKIMTSIN 320
   ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 11

US-08-748-506-13

; Sequence 13, Application US/08748506

; Patent No. 6159707

; GENERAL INFORMATION:

; APPLICANT: Ronnett et al.

; TITLE OF INVENTION: NOVEL SPERM RECEPTORS

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leydig, Voit & Mayer, Ltd.

; STREET: Two Prudential Plaza, Suite 4900

; CITY: Chicago

; STATE: IL

; COUNTRY: US

; ZIP: 60601-6780

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-748-506-13

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```

Query Match      38.7%; Score 653; DB 4; Length 321;
Best Local Similarity 46.5%; Pred. No. 6.1e-51;
Matches 133; Conservative 43; Mismatches 106; Indels 4; Gaps 1;

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QY 27 LLEFLSLDYLVLVTENMLIIIRNHPFLHAKPMYFFLANMSFLEIYYVTITPKMLAGF 86
   ||| ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 32 LLEFLTLMLFVLSTGNALALACTSPSLHTPMYFFLANLSLEIGYCSVIPKMLQSL 91
   ||| ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 87 IGSKENHGOLISFEACMTOLYFFLGCTECVLLAVMADRYVAIGHPLHYPIVSRIC 146
   : ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 92 VSEAREITFV---GATQMEFFTFGITECCLLAAMAEFRMGICSPHYATRMSREVC 147
   : ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 147 VQMAAGSMAGFGISWVKYFELISRLSYCGPNTINHFCDVSPLLNLCSTDMSTAEITDFV 206
   : ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 148 AHLAIYSWMGCIYGLQGTNNIISLNFCCGEIDHFFCDLPPLALACDTSQNEAIEFV 207
   : ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 207 LAIFILLGPLSVGASYMAITGAVMRIPSAAGRHKAFTSCASHLYVIIIFYASITFYAR 266
   : ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 208 VVVLICISPELVLYSYVRLVAVLWVPSEGRHKALSTCSSHLVLTLYFGSVSTFYLR 267
   : ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 267 PKALSAFDNTKLIVSYAVIVPLFNPIIYCLRNODVKRALRRLTLHL 312
   ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 268 PKSSHSPGMDKLALFTYATVTSMLNPIIYSLRNKDYKALRLTLAL 313
   ||| : : : ||| : : ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 12

US-08-748-506-24

; Sequence 24, Application US/08748506

; Patent No. 6159707

; GENERAL INFORMATION:

; APPLICANT: Ronnett et al.

; TITLE OF INVENTION: NOVEL SPERM RECEPTORS

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leydig, Voit & Mayer, Ltd.

; STREET: Two Prudential Plaza, Suite 4900

; CITY: Chicago

; STATE: IL

; COUNTRY: US

; ZIP: 60601-6780

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25



CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/748, 506  
FILING DATE: 08-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/033, 751  
FILING DATE: 09-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
REFERENCE/DOCKET NUMBER: 74940  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5700  
TELEFAX: 312-616-5600  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 327 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-748-506-24

Query Match 37.6%; Score 633.5; DB 4; Length 327;  
Best Local Similarity 42.0%; Pred. No. 3,4e-49;  
Matches 132; Conservative 51; Mismatches 122; Indels 9; Gaps 2;  
QY 10 VSEVLGEPAPAPRLVFLSLDYLVLTEENMLIIIRNHPPTLHKPMYFFLANMSF 69  
DB 15 VQELFEGFPAEHRILFLLHMLAYLASSGMNLIITTCVDRLQTPMFFLSTFSF 74  
QY 70 LEIMVYVITPKMLAGFSGKENHGOLISFEACMTOLYFELGCTECVLLAAMAYDRYV 129  
DB 75 VECFEITVITPOLITLISGR----QKIPMACFSQAFVVLFLGAAYFFLAVALSLDRFL 130  
QY 130 AICHPAYIVVSRCLCYMAAGSGEISWVKVFLISRLSYCGPNTIHFFCDVSPL 189  
DB 131 AICRPLHYPTIMSPMCFLLVTVSLVGLFPMASPVVMLQSFCGPNIIHFFCDGFL 190  
QY 190 LNLSTGDAELDFVLAIFLLGLPLSVTGASYMATIGAMRIPSAGRKAPSTCSH 249  
DB 191 ANLSQSESRSTEMLEFLLATVLTSLIAIPASTVITVTLPSAERORAPSTCSH 250  
QY 250 LTVIIFAAISFIYARPKALSAFTNKLVSVLAVIPLFNPIIYCLRNODVYKALRRT 309  
DB 251 LIVLSLMGSCVFIYAKKORSVDNREAVLVNMVYPLNPIYITLRNQNQVALDA 310  
QY 310 -----LHLAQDEA 318  
DB 311 LSRVOLHRYGSRKA 324

RESULT 13  
US-08-748-506-14  
Sequence 14, Application US/08748506  
Patent No. 6159707  
GENERAL INFORMATION:  
APPLICANT: Ronnett et al.  
TITLE OF INVENTION: NOVEL SPERM RECEPTORS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Volt & Mayer, Ltd.  
STREET: Two Prudential Plaza, Suite 4900  
CITY: Chicago  
STATE: IL  
COUNTRY: US  
ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/748, 506

FILING DATE: 08-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/033, 751  
FILING DATE: 09-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
REFERENCE/DOCKET NUMBER: 74940  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5600  
TELEFAX: 312-616-5700  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 327 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-748-506-14

Query Match 37.0%; Score 623.5; DB 4; Length 327;  
Best Local Similarity 41.2%; Pred. No. 2,7e-48;  
Matches 129; Conservative 53; Mismatches 126; Indels 5; Gaps 2;  
QY 2 ERNHSGRVSEFVLLGFPAPAPRLVFLSLDYLVLTEENMLIIIRNHPPTLHKPMY 61  
DB 8 ETRNGT-LVLEFILLEGVAAEHLKLFLLHMLAYLASSGMNLIITTCVDRLQTPMY 66  
QY 62 FFLANMSFLEIMVYVITPKMLAGFSGKENHGOLISFEACMTOLYFELGCTECVLLA 121  
DB 67 FFLTSFVECCFITTAIPOLLITLISGR----QKIPGVCFSQAFVVLVGAGGFLLA 122  
QY 122 VMAYDRIYATCHPLHYPIYVSSRLCYMAAGSGEISWVKVFLISRLSYCGPNTIH 181  
DB 123 ALSDFPLAICKPLHYPTIMSPMCFLLVTVCLFGLFPMASPVVMLSKTFYCGPNIIH 182  
QY 182 FECDVSPPLNLSCTDMASAEITDFVLAIFLLGLPLSVTGASYMATIGAMRIPSAGRK 241  
DB 183 FFCDDGPLANISCSERTREIMLEFLLAVIYFASFLIAIFASINVIYIVLPSAEROR 242  
QY 242 AFTCSAHLVYVIFAAISFIYARPKALSAFTNKLVSVLAVIPLFNPIIYCLRNOD 301  
DB 243 AFTSCSSHLIYLSLMYGCATLYLKPKORSVDNREAVLVNMVYPLNPIYITLRNQ 302  
QY 302 VKRALRRTLHLAQ 314  
DB 303 VHQALRDLASRLQ 315

RESULT 14  
US-08-988-876-7  
Sequence 7, Application US/08988876  
Patent No. 6063596  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Bandman, Olga  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED  
WITH IMMUNE RESPONSE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Inocyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,876  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0441 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 314 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 32086  
US-08-988-876-7

Query Match 36.9%; Score 623; DB 3; Length 314;  
Best Local Similarity 42.4%; Pred. No. 2,8e-48;  
Matches 128; Conservative 56; Mismatches 114; Indels 4; Gaps 1;

QY 10 VSEFVLGPPAPAPRLVLLFFSLDYLVTENMLIIAIRNHPPLHKKPMYFLLANMSF 69  
DB 9 ISDFLLGIPQEQONLCYALFLAMVLTLLGNLLIIVLRDLSHLTPMYFLSLMSF 68  
QY 70 LEIWTYVTPKMLAGFISGENHGOISPEACMTQYFELGSGTECVLLAMAYDRY 129  
DB 69 SDCEFSVTIPKLLQ---NMQNDPSIPADCTQMYFELGSGTECVLLAMAYDRY 124  
QY 130 AICPLHPIYVYSSRLCYVMAAGSGFGISNWKVFLISRLSYCGPNTINHEFCVSP 189  
DB 125 AICFPLHYTAIYMSRMLCLVALSVLTTFHMLHTLMARLCFCADVTPHFCDMSAL 184  
QY 190 LNSCTDMSTAEITDVLAIFILGPLSVTGASYMAITGAVMRIPSAAGRHKAFSTCASH 249  
DB 185 LKLAFTDRNENVIIMGGLIIVIPFLILGSIYARIVSSILKVPSSKICKAFSTCGSH 244  
QY 250 LFWIIFVYASIFIVARPKLASFDTNKLVSVLYAVIPLFNPIICLRNODVKKALRRT 309  
DB 245 LSVSLFTGIVIGLYLCCSANSSTLKTQVAMMYTVTPMLNPFITSLRNDRMGALSRV 304  
QY 310 LHLAQ 314  
DB 305 LSRVQ 306

RESULT 15  
US-08-748-506-22  
Sequence 22, Application US/08748506  
Patent No. 6159707  
GENERAL INFORMATION:  
APPLICANT: Ronnelt et al.  
TITLE OF INVENTION: NOVEL SPERM RECEPTORS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Voigt & Mayer, Ltd.  
STREET: Two Prudential Plaza, Suite 4900  
CITY: Chicago  
STATE: IL  
COUNTRY: US  
ZIP: 60601-6780  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/748,506  
FILING DATE: 08-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/033,751  
FILING DATE: 09-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
REFERENCE/DOCKET NUMBER: 74940  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5700  
TELEFAX: 312-616-5600  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 327 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-748-506-22

Query Match 36.5%; Score 616; DB 4; Length 327;  
Best Local Similarity 42.0%; Pred. No. 1.3e-47;  
Matches 128; Conservative 50; Mismatches 123; Indels 4; Gaps 1;

QY 10 VSEFVLGPPAPAPRLVLLFFSLDYLVTENMLIIAIRNHPPLHKKPMYFLLANMSF 69  
DB 15 VLEFIIDRFVABHLIFELFLHLAVLSLGMNMLITTCVDHRLQTPMYFLLMSFSS 74  
QY 70 LEIWTYVTPKMLAGFISGENHGOISPEACMTQYFELGSGTECVLLAMAYDRY 129  
DB 75 VECCFITTVIPQLITILSR----OKIPMAISQAFYLVVGATGFLVGLSLDRFL 130  
QY 130 AICPLHPIYVYSSRLCYVMAAGSGFGISNWKVFLISRLSYCGPNTINHEFCVSP 189  
DB 131 AICFPLHYTAIYMSRMLCLVALSVLTTFHMLHTLMARLCFCADVTPHFCDGSP 190  
QY 190 LNSCTDMSTAEITDVLAIFILGPLSVTGASYMAITGAVMRIPSAAGRHKAFSTCASH 249  
DB 191 ANLSCSETRSIEMLEFTLAIIVPASLLAIFAYSNIVTVIPLPARERORAFSTCASH 250  
QY 250 LFWIIFVYASIFIVARPKLASFDTNKLVSVLYAVIPLFNPIICLRNODVKKALRRT 309  
DB 251 LIVLSMTGSCATITLAKPKORSRVDINREALVNTVTPILNVIYITLRNKKVHQALRDA 310  
QY 310 LHLAQ 314  
DB 311 LSRVQ 315

Search completed: May 22, 2002, 15:40:20  
Job time: 565 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 22, 2002, 15:33:51 ; Search time 29.43 Seconds  
(without alignments)  
1922.166 Million cell updates/sec

Title: US-09-771-209-76  
Perfect score: 1687  
Sequence: 1 MERRHNSGVSEFVLLGFPA.....RTLLHLAQDEANTNKGSKIG 327

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPREMBL\_19:\*  
2: sp\_archaea:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1613	95.6	327	11	Q9QWU6
2	1498	88.8	327	4	Q9H206
3	988	58.6	316	11	Q9EPG2
4	975	57.8	316	11	Q9EPG1
5	970	57.5	316	11	Q9EPV0
6	956.5	56.7	323	13	Q57597
7	931.5	55.2	323	13	Q13036
8	741	43.9	307	11	Q9EPV1
9	739	43.8	222	13	P70024
10	738	43.7	307	11	Q9EPG7
11	735	43.6	307	11	Q9EPG9
12	732.5	43.4	324	11	Q9WU86
13	727.5	43.1	315	11	Q9JKA6
14	722	42.8	307	11	Q9EPG0
15	720	42.7	215	4	Q96R38
16	717.5	42.5	317	11	Q9EPG3

17	717.5	42.5	324	11	Q920G5	Q920G5 mus musculus
18	710.5	42.1	317	11	Q9EPG4	Q9EPG4 mus musculus
19	708	42.0	306	4	Q96KA4	Q96KA4 homo sapien
20	705.5	41.8	317	4	Q9H208	Q9H208 homo sapien
21	696.5	41.3	319	11	Q9QZ22	Q9QZ22 mus musculus
22	695.5	41.2	314	11	Q9EPG6	Q9EPG6 mus musculus
23	694.5	41.2	310	11	Q9EP55	Q9EP55 mus musculus
24	690	40.9	267	11	Q9EPX6	Q9EPX6 mus musculus
25	688	40.8	319	11	Q9QZ19	Q9QZ19 mus musculus
26	682	40.4	314	11	Q9EPG5	Q9EPG5 mus musculus
27	680.5	40.3	312	11	Q9EPG8	Q9EPG8 gallus gall
28	679	40.2	313	11	Q63394	Q63394 rattus norv
29	678.5	40.2	317	11	Q923R1	Q923R1 mus musculus
30	675.5	40.0	318	11	Q9QZ21	Q9QZ21 mus musculus
31	675	40.0	318	11	Q9QZ20	Q9QZ20 mus musculus
32	674	40.0	267	11	Q9EPX7	Q9EPX7 rattus norv
33	673.5	39.9	312	11	Q9QZ18	Q9QZ18 mus musculus
34	673	39.9	318	11	Q920Z2	Q920Z2 mus musculus
35	672	39.8	314	6	077756	077756 pan troglod
36	669.5	39.7	313	6	077758	077758 hylobates l
37	667.5	39.6	308	13	Q9QX09	Q9QX09 ambystoma t
38	667.5	39.6	313	11	Q9Z1V0	Q9Z1V0 mus musculus
39	666.5	39.5	312	11	Q9EPG0	Q9EPG0 gallus gall
40	666	39.5	315	11	Q35434	Q35434 rattus norv
41	666	39.5	321	11	070266	070266 rattus norv
42	664	39.4	312	13	Q9QX10	Q9QX10 ambystoma t
43	662	39.2	129	11	Q9ESG0	Q9ESG0 mus musculus
44	661	39.2	308	11	Q9R0K3	Q9R0K3 mus musculus
45	661	39.2	321	11	070268	070268 rattus norv

## ALIGNMENTS

RESULT 1  
ID Q9QWU6 PRELIMINARY; PRT; 327 AA.  
AC Q9QWU6;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE OLFACTORY RECEPTOR 17.  
OS OLFR41.  
GN Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SRRAIN-BL/6;  
RA MEDLINE=99091050; PubMed=9875846;  
RA Krautwurst D., Yau K.W., Reed R.R.;  
RT "Identification of ligands for olfactory receptors by functional  
RT expression of a receptor library."  
RL Cell 95:917-926(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SVJ;  
RA Lane R.P., Cutforth T., Young J., Athanasios M., Friedman C.,  
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;  
RT "Genomic Analysis of Orthologous Mouse and Human Olfactory Receptor  
RT Loci Indicates Cluster Stability yet Minimal Conservation Beyond the  
RT Coding Sequence."  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF106007; ADI3307.1; -;  
DR EMBL: AF312133; AAG45187.1; -;  
DR MGI: 1333840; Olfr41.  
DR Interpro: IPR000276; GPCR\_Rhodopsin.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
DR PROSITE: PS00237; G\_PROTEIN\_RECPT\_F1\_1; UNKNOWN.1.  
DR PROSITE: PS50262; G\_PROTEIN\_RECPT\_F1\_2; 1.  
KW Receptor.

SEQUENCE 327 AA; 36150 MW; 4E94C75C909210E5 CRC64;

Query Match 95.6%; Score 1613; DB 11; Length 327;

Best Local Similarity 95.1%; Pred. No. 1.2e-145; Mismatches 311; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

```

OY 1 MERRNHSRVSEFVLLGFAPAPAPLRLVFLSLDYLVLVTENMLIIAIRNHPYLHKPM 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MERRNHTGRVSEFVLLGFAPAPAPLRLVFLSLDYLVLVTENMLIIAIRNHPYLHKPM 60
OY 61 YFFLAMSFLEIYVTVITPKMLAGFISGENHGOLISFEACMTOLYFELGCTECVLL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 YFFLAMSFLEIYVTVITPKMLAGFISGENHGOLISFEACMTOLYFELGCTECVLL 120
OY 121 AVAYADRYVAICHPHYPIVSSRLCVQMAAGSMAGGFGISMKVFLISRLSYCGPNTIN 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 AVAYADRYVAICHPHYPIVSSRLCVQMAAGSMAGGFGISMKVFLISRLSYCGPNTIN 180
OY 181 HFFCDVSPLLNSTCTDMSTAEITDFVLAIFILGLPSVTGASYMAITGAVMRIPSAAGR 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 HFFCDVSPLLNSTCTDMSTAEITDFVLAIFILGLPSVTGASYMAITGAVMRIPSAAGR 240
OY 241 KAFSTCASHLTVTIITYAASIFIYARPKALSADTKLVSLYAVIVPLNPIITCLRNQ 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 241 KAFSTCASHLTVTIITYAASIFIYARPKALSADTKLVSLYAVIVPLNPIITCLRNQ 300
OY 301 DYKRALRRTLHLAODEANTNGSKIG 327
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 301 EYVKALRRTLHLAOGODANTNGSKSRDG 327

RESULT 2
OY 09H206 PRELIMINARY; PRT; 327 AA.
AC 09H206:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HIT OLFACTOR RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21310002; PubMed=11416212;
RA Lane R.P., Cutforth T., Young J., Athanasios M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic analysis of orthologous mouse and human olfactory receptor
RT loci."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
DR EMBL; AF321237; AAG45208.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 327 AA; 36154 MW; 9C11914D3F069FC1 CRC64;

```

Query Match 88.8%; Score 1498; DB 4; Length 327;  
Best Local Similarity 89.5%; Pred. No. 1.1e-134;  
Matches 291; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

```

OY 1 MERRNHSRVSEFVLLGFAPAPAPLRLVFLSLDYLVLVTENMLIIAIRNHPYLHKPM 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MERRNHSRVSEFVLLGFAPAPAPLRLVFLSLDYLVLVTENMLIIAIRNHPYLHKPM 60
OY 61 YFFLAMSFLEIYVTVITPKMLAGFISGENHGOLISFEACMTOLYFELGCTECVLL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 YFFLAMSFLEIYVTVITPKMLAGFISGENHGOLISFEACMTOLYFELGCTECVLL 120

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```

OY 121 AVAYADRYVAICHPHYPIVSSRLCVQMAAGSMAGGFGISMKVFLISRLSYCGPNTIN 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 AVAYADRYVAICHPHYPIVSSRLCVQMAAGSMAGGFGISMKVFLISRLSYCGPNTIN 180
OY 181 HFFCDVSPLLNSTCTDMSTAEITDFVLAIFILGLPSVTGASYMAITGAVMRIPSAAGR 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 HFFCDVSPLLNSTCTDMSTAEITDFVLAIFILGLPSVTGASYMAITGAVMRIPSAAGR 240
OY 241 KAFSTCASHLTVTIITYAASIFIYARPKALSADTKLVSLYAVIVPLNPIITCLRNQ 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 241 KAFSTCASHLTVTIITYAASIFIYARPKALSADTKLVSLYAVIVPLNPIITCLRNQ 300
OY 301 DYKRALRRTLHLAODEANTNGSK 325
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 301 EYVKALRRTLHLAODEANTNGSKSR 325

```

```

RESULT 3
OY 09EPG2 PRELIMINARY; PRT; 314 AA.
AC 09EPG2:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE M51 OLFACTOR RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=C57BL/6J; PubMed=11416212;
RA Lane R.P., Cutforth T., Young J., Athanasios M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic analysis of orthologous mouse and human olfactory receptor
RT loci."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
DR EMBL; AF321234; AAG45189.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 314 AA; 35713 MW; 9E0AFB9E7F1D8CC7 CRC64;

```

Query Match 58.6%; Score 988; DB 11; Length 314;  
Best Local Similarity 59.5%; Pred. No. 4.1e-86;  
Matches 179; Conservative 60; Mismatches 58; Indels 4; Gaps 1;

```

OY 10 VSEFVLLGFAPAPAPLRLVFLSLDYLVLVTENMLIIAIRNHPYLHKPMYFFLAMSF 69
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 9 VSEFVLLGFAPAPAPLRLVFLSLDYLVLVTENMLIIAIRNHPYLHKPMYFFLAMSF 68
OY 70 LEIYVTVITPKMLAGFISGENHGOLISFEACMTOLYFELGCTECVLLAVMAYDRYV 129
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 69 LEIYVTVITPKMLAGFISGENHGOLISFEACMTOLYFELGCTECVLLAVMAYDRYV 124
OY 130 ATCHPLRYPIVSSRLCVQMAAGSMAGGFGISMKVFLISRLSYCGPNTINHFFCDVSP 189
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 125 ATCHPLRYPIVSSRLCVQMAAGSMAGGFGISMKVFLISRLSYCGPNTINHFFCDVSP 184
OY 190 LNSTCTDMSTAEITDFVLAIFILGLPSVTGASYMAITGAVMRIPSAAGRHAFTCASH 249
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 185 LNSTCTDMSTAEITDFVLAIFILGLPSVTGASYMAITGAVMRIPSAAGRHAFTCASH 244
OY 250 LTVIITYAASIFIYARPKALSADTKLVSLYAVIVPLNPIITCLRNQDYKRALRRT 309
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 245 LTVIITYAASIFIYARPKALSADTKLVSLYAVIVPLNPIITCLRNQDYKRALRRT 304

```

	RESULT	
Q9EPV0	5	
O9EPV0		PRELIMINARY; PRT; 316 AA.
AC O9EPV0;		
DT 01-MAR-2001	(Tremblrel, 16, Created)	
DT 01-MAR-2001	(Tremblrel, 16, Last sequence update)	
DT 01-DEC-2001	(Tremblrel, 19, Last annotation update)	
DE M50	OLFACTORY RECEPTOR (OLFATORY RECEPTOR M50).	

DT 01-JUN-1998 (TREMblrel. 06, last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
DE CHICK OLFACtORY RECEPTOR 7.  
GN COR7A.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.

OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE OF 1-319 FROM N.A.  
 RX MEDLINE=96317247; PubMed=8734500;  
 RA Nef S., Allaman I., Plumell H., De Castro E., Nef P.;  
 RT "Olfaction in birds: differential embryonic expression of nine  
 RT putative odorant receptor genes in the avian olfactory system";  
 RL Mech. Dev. 53:65-77(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Nef S., Allaman I., De Castro E., Nef P.;  
 RT "Transient expression of cor7b, a putative odorant receptor gene, in  
 RT the notochord";  
 RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z79586; CAB01847.1; -.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECIP\_FL\_1; UNKNOWN\_1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECIP\_FL\_2; 1.  
 DR Receptor: G-protein coupled receptor.  
 KW Receptor: G-protein coupled receptor.  
 SQ SEQUENCE 323 AA; 36670 MW; 8A0D48EA7EB35888 CRC64;

## Query Match

Best Local Similarity 55.7%; Score 956.5; DB 13; Length 323;  
 Matches 173; Conservative 63; Mismatches 69; Indels 5; Gaps 2;

OY 1 MERRNSGRVSEVFLGFAPAPARVLFFLLSDVVLVTENMLIIAIRNPTLHKRP 60  
 DB 1 MERRNSGRVSEVFLGFAPAPARVLFFLLSDVVLVTENMLIIAIRNPTLHKRP 59  
 OY 61 YFFLAMSFLEIYVVTTPKMLAGFISKENHGLISFACMTQLYFFLGCTECVLL 120  
 DB 61 YFFLAMSFLEIYVVTTPKMLAGFISKENHGLISFACMTQLYFFLGCTECVLL 115  
 OY 121 AVAYDRVVAICPLHYPIVIVSRCLCVQMAAGSGFGISMKVFLISRLSYCGPNTN 180  
 DB 121 AVAYDRVVAICPLHYPIVIVSRCLCVQMAAGSGFGISMKVFLISRLSYCGPNTN 175  
 OY 116 SAMAYDRVVAICPLHYPIVIVSRCLCVQMAAGSGFGISMKVFLISRLSYCGPNTN 175  
 DB 116 SAMAYDRVVAICPLHYPIVIVSRCLCVQMAAGSGFGISMKVFLISRLSYCGPNTN 175  
 OY 181 HFFCDVSPPLNLSCTDMSAELTDFVLAIFILLGPLSVTGASYMATGAVMRIPSAGRH 240  
 DB 181 HFFCDVSPPLNLSCTDMSAELTDFVLAIFILLGPLSVTGASYMATGAVMRIPSAGRH 235  
 OY 241 KAFSTCASHLTAVIIFVAFSIFVYAPRKALSAFTNKLVSVLAVVLPFNPIIYCLRNQ 300  
 DB 241 KAFSTCASHLTAVIIFVAFSIFVYAPRKALSAFTNKLVSVLAVVLPFNPIIYCLRNQ 295  
 OY 301 DVKRALRTL 310  
 DB 301 DVKRALRTL 305  
 DB 296 ELKRAFKKAL 305

RESULT 7  
 ID 013036 PRELIMINARY: PRT: 323 AA.  
 AC 013036:  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CHICK OLFACTORY RECEPTOR 7.  
 GN COR7B.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE OF 1-319 FROM N.A.  
 RX MEDLINE=96317247; PubMed=8734500;  
 RA Nef S., Allaman I., Plumell H., De Castro E., Nef P.;  
 RT "Olfaction in birds: differential embryonic expression of nine  
 RT putative odorant receptor genes in the avian olfactory system";  
 RL Mech. Dev. 53:65-77(1996).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97272300; PubMed=9114066;  
 RA Nef S.S., Nef P.N.;  
 RT "Olfaction: Transient expression of cor7b, a putative odorant receptor  
 RT gene, in the notochord during early stages of development";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4766-4771(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Nef S.;  
 RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z79587; CAB01848.1; -.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECIP\_FL\_1; UNKNOWN\_1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECIP\_FL\_2; 1.  
 DR Receptor: G-protein coupled receptor.  
 KW Receptor: G-protein coupled receptor.  
 SQ SEQUENCE 323 AA; 36686 MW; DDEB4585A971920 CRC64;

## Query Match

Best Local Similarity 55.2%; Score 931.5; DB 13; Length 323;  
 Matches 170; Conservative 62; Mismatches 73; Indels 5; Gaps 2;

OY 1 MERRNSGRVSEVFLGFAPAPARVLFFLLSDVVLVTENMLIIAIRNPTLHKRP 60  
 DB 1 MERRNSGRVSEVFLGFAPAPARVLFFLLSDVVLVTENMLIIAIRNPTLHKRP 59  
 OY 61 YFFLAMSFLEIYVVTTPKMLAGFISKENHGLISFACMTQLYFFLGCTECVLL 120  
 DB 61 YFFLAMSFLEIYVVTTPKMLAGFISKENHGLISFACMTQLYFFLGCTECVLL 115  
 OY 121 AVAYDRVVAICPLHYPIVIVSRCLCVQMAAGSGFGISMKVFLISRLSYCGPNTN 180  
 DB 121 AVAYDRVVAICPLHYPIVIVSRCLCVQMAAGSGFGISMKVFLISRLSYCGPNTN 175  
 OY 116 SAMAYDRVVAICPLHYPIVIVSRCLCVQMAAGSGFGISMKVFLISRLSYCGPNTN 175  
 DB 116 SAMAYDRVVAICPLHYPIVIVSRCLCVQMAAGSGFGISMKVFLISRLSYCGPNTN 175  
 OY 181 HFFCDVSPPLNLSCTDMSAELTDFVLAIFILLGPLSVTGASYMATGAVMRIPSAGRH 240  
 DB 181 HFFCDVSPPLNLSCTDMSAELTDFVLAIFILLGPLSVTGASYMATGAVMRIPSAGRH 235  
 OY 241 KAFSTCASHLTAVIIFVAFSIFVYAPRKALSAFTNKLVSVLAVVLPFNPIIYCLRNQ 300  
 DB 241 KAFSTCASHLTAVIIFVAFSIFVYAPRKALSAFTNKLVSVLAVVLPFNPIIYCLRNQ 295  
 OY 301 DVKRALRTL 310  
 DB 301 DVKRALRTL 305  
 DB 296 ELKRAFKKAL 305

RESULT 8  
 ID 09EPV1 PRELIMINARY: PRT: 307 AA.  
 AC 09EPV1:  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE B6 OLFACTORY RECEPTOR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129SVJ;  
 RX MEDLINE=21310002; PubMed=11416212;  
 RA Lane R.P., Curforth T., Young J., Athanasios M., Friedman C.,  
 RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;  
 RT "Genomic analysis of orthologous mouse and human olfactory receptor  
 RT loci";  
 RT Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).  
 RL EMBL; AF321235; AAG45201.1; -.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.







QY 10 VSEFVLLGFAPAPLRVLLFFLSLDYVLVTENMLIIAIRNHP TLHKPMYFFLANMSF 69



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:19:09 ; Search time 32.83 Seconds  
(Without alignments)  
1106.340 Million cell updates/sec

Title: US-09-771-209-76  
Perfect score: 1687  
Sequence: 1 MERRHSGRVSFVLLGPPA.....RTLHLAQDEANTNGSKIG 327

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: A.Geneseq.032802.\*  
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*  
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.\*  
9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.\*  
10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.\*  
11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.\*  
12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.\*  
13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.\*  
14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.\*  
15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.\*  
16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.\*  
17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.\*  
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB ID	Description
1	1671	99.1	327	13	AA27872
2	1490	88.3	327	22	AAU24727
3	1454	86.2	327	22	AA271675
4	1395	82.7	327	22	AA271683
5	1382.5	82.0	286	15	AA48744
6	1382.5	82.0	286	17	AAW02716
7	1248	74.0	278	22	AA272010
8	1248	74.0	278	22	AA272365
9	971.5	57.6	317	22	AAU24722
10	970.5	57.5	317	22	AA271777
11	957.5	56.8	301	22	AA265357

12	957.5	56.8	311	22	AA271414	Human olfactory re
13	957.5	56.8	311	22	AA272361	Human OR-like poly
14	944.5	56.0	324	22	AA271590	Human olfactory re
15	944.5	56.0	324	22	AA272479	Human OR-like poly
16	944.5	56.0	325	22	AA274639	Human olfactory re
17	923	54.7	314	22	AA271962	Human olfactory re
18	887	52.6	319	22	AA271967	Human olfactory re
19	871	51.6	330	22	AA272645	Murine OR-like pol
20	788	46.7	311	22	AA273006	Olfactory receptor
21	784	46.5	311	13	AA27869	Odorant receptor c
22	776	46.0	317	22	AA274626	Human olfactory re
23	776	46.0	317	22	AA271729	Human olfactory re
24	776	46.0	317	22	AA272467	Human OR-like poly
25	774	45.9	308	22	AA274700	Human olfactory re
26	774	45.9	308	22	AA271889	Human olfactory re
27	766.5	45.4	291	22	AA271807	Human olfactory re
28	752.5	44.6	312	22	AA271811	Novel human diagno
29	751	44.5	312	22	AA273032	Human olfactory re
30	750.5	44.5	317	22	AA271814	Olfactory receptor
31	745.5	44.2	312	22	AA274609	Human olfactory re
32	745.5	44.2	312	22	AA272585	Human G-protein co
33	745.5	44.2	312	22	AA272585	Human OR-like poly
34	743	44.0	304	22	AA271480	Human olfactory re
35	743	44.0	304	22	AA272579	Human OR-like poly
36	743	44.0	312	22	AA274601	Human olfactory re
37	739	43.8	222	22	AA273062	Olfactory receptor
38	738	43.7	304	22	AA266385	Murine partial olf
39	736	43.6	317	22	AA271824	Human olfactory re
40	733.5	43.5	317	22	AA271931	Human olfactory re
41	733.5	43.5	322	22	AA274728	Human olfactory re
42	730.5	43.3	314	22	AA205133	Human odorant rece
43	730.5	43.3	314	22	AA271581	Human olfactory re
44	730	43.3	324	22	AA271913	Human G-protein co
45	730	43.3	324	22	AA274667	Human olfactory re

ALIGNMENTS

RESULT 1	
AA27872	standard; Protein; 327 AA.
XX	
XX	
AC	AA27872: (first entry)
XX	
DT	15-MAR-1993
XX	
XX	
DE	Odorant receptor clone 17.
XX	
KW	Odorant receptor; Insect; vertebrate; fish; mammal; neurotransmitter;
KW	hormone; G-protein; surface receptor; olfactory epithelium; PCR;
KW	Sprague-Dawley rat; amplify; primer; polymerase chain reaction;
KW	multigene family; ligand binding domain.
XX	
OS	Rattus rattus.
XX	
FT	Key MISC-difference 35
FT	Location/Qualifiers
FT	/Label= VAL, ALA, ASP, GLY
XX	
PN	W09217585-A.
XX	
PD	15-OCT-1992.
XX	
PE	06-APR-1992: 92WO-US02741.
XX	
PR	05-APR-1991: 91US-0681880.
XX	
PA	(UYCO ) UNIV COLUMBIA NEW YORK.
XX	
PI	Axel R, Buck LB;
XX	
DR	WPI: 1992-366257/44.

DR N-PSDB: AA029860.  
XX Nucleic acid encoding an odorant receptor - can be used to  
PT control insect populations or for detecting odours e.g. alcohol,  
PT explosives, natural gas etc.

PS Claim 41; Fig 14; 195pp; English.

XX The sequences given in AAR27867-89 are encoded by odorant receptor  
CC clones derived from an insect, a vertebrate, a fish or a mammal.  
CC These clones form a family of neurotransmitters and hormone receptors  
CC which transduce intracellular signals by activation of specific G-  
CC proteins. Each of these receptors is a member of a superfamily of  
CC surface receptors which traverse the membrane seven times. These  
CC clones are only expressed in the olfactory epithelium. These clones  
CC were isolated using probes derived from RNA prepared from the  
CC olfactory epithelia of Sprague-Dawley rats. Isolated cDNA's were  
CC amplified using primers which correspond to transmembrane domain 2  
CC and 7. PCR products of the appropriate size were isolated and  
CC sequenced. The deduced protein sequences of these cDNA's defined a  
CC new multigene family which shared sequence and structural properties  
CC with the superfamily of neurotransmitter and hormone receptors which  
CC traverse the membrane seven times. This novel family, however  
CC exhibits features different from any other member of the superfamily  
CC identified so far. There is a striking divergence within the third,  
CC fourth and fifth transmembrane domains between the olfactory proteins.  
CC This divergence in the potential ligand binding domain is consistent  
CC with the idea that the family of molecules cloned is capable of  
CC associating with a large number of odorant of diverse molecular  
CC structure.

XX Sequence 327 AA:

Query Match 99.1%; Score 1671; DB 13; Length 327;

Best Local Similarity 99.1%; Pred. No. 3.7e-187; Mismatches 2; Indels 0; Gaps 0;

Matches 324; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MERRHSGVSEFVLLGPPAPAPLAVLLEFSLDYLVLVTENMLITAIRNHPTLHKPM 60  
DB 1 mertrhsgvsefvlllgfpapaplvllffllslxyvlvtlenmlitairnhptlhkpm 60  
QY 61 YFFLANMSFLEIWTYVTPKMLAGFIGSKENHGOLISFEACMTOLYFFLGCTECVLL 120  
DB 61 yfflanmsflelwtvtpkmlagfigskenhgqlisfeacmtqlyffligctecvll 120  
QY 121 AVMAVDYVAICHPPLHYPIYVSSRLCVQMAAGSWAGFGISMKVYKVELISRLSYCGPNTIN 180  
DB 121 avmaydryvaichpplhyvpyivssrlcvqmaagswagfgismkvkvelisrlsygcpntln 180  
QY 181 HFFCQVSPULNISCCTDMSTAEITDFVLAIFILGLPSTVGASYMAITGAVMRIPSAAGR 240  
DB 181 hffcdvspulniscctdmstaeltfdvllaifilglpstvgaasymaitgavmrpsaagrh 240  
QY 241 KAFSTCASHLTWVITFYVASTFIYARPKALSAFDNKLVSIVYAVIVPFFNFITICLRNQ 300  
DB 241 kafstcashltwvltfyvastsfiyarpkalsafdnklvsvlyavivpffnfiycltnq 300  
QY 301 DVKRALRRTLHLADQDEANTNGSKIG 327  
DB 301 dvkralrtrtlhlaqdqeantngsklg 327

RESULT 2  
ID AAU24727 standard; Protein; 327 AA.

AC AAU24727;  
XX 18-DEC-2001 (first entry)  
XX Human olfactory receptor AOLF226.  
XX

KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odorant;  
KW food additive; cosmetic; fragrance; pharmaceutical additive.  
OS Homo sapiens.  
XX WO200168805-A2.  
XX

PD 20-SEP-2001.

XX 13-MAR-2001; 2001WO-US07771.

XX 13-MAR-2000; 2000US-0188914.

PR 24-MAR-2000; 2000US-0192033.

PR 12-APR-2000; 2000US-0196474.

PR 24-APR-2000; 2000US-0199335.

PR 26-MAY-2000; 2000US-0207702.

PR 23-JUN-2000; 2000US-0213849.

PR 16-AUG-2000; 2000US-0226534.

PR 07-SEP-2000; 2000US-0230732.

PR 07-FEB-2001; 2001US-0266862.

PA (SENO-) SENOMYX INC.

PI Zozulya S:

XX WPI: 2001-570867/64.

XX N-PSDB: AAS42420.

XX Nucleic acids encoding human olfactory G protein-coupled receptors,

XX useful for screening for compounds involved in olfactory sensation,

XX where the compounds can be used in the food, pharmaceutical and

XX cosmetic industries to customise odours -

XX Claim 60; Page 178; 319pp; English.

XX The invention relates to nucleic acids encoding human olfactory

XX receptors, OR, (a G protein-coupled receptor, GPCR). The OR's

XX specifically recognise molecules, odorants, that elicit specific

XX olfactory sensation. The human olfactory receptors and polynucleotides

XX encoding them are useful for screening a library of chemical compounds

XX for compounds that are involved in olfactory sensation. Modulators of

XX their activity are useful for pharmacological and genetic modulation of

XX olfactory signalling pathways. Therefore, they can be used in the food,

XX pharmaceutical and cosmetic industries to customise odours and

XX fragrances. The present sequence is a human olfactory receptor of the

XX invention.

XX Sequence 327 AA:

Query Match 88.3%; Score 1490; DB 22; Length 327;

Best Local Similarity 89.2%; Pred. No. 6.2e-166; Mismatches 21; Indels 0; Gaps 0;

Matches 290; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 MERRHSGVSEFVLLGPPAPAPLAVLLEFSLDYLVLVTENMLITAIRNHPTLHKPM 60  
DB 1 mertrhsgvsefvlllgfpapaplvllffllslxyvlvtlenmlitairnhptlhkpm 60  
QY 61 YFFLANMSFLEIWTYVTPKMLAGFIGSKENHGOLISFEACMTOLYFFLGCTECVLL 120  
DB 61 yfflanmsflelwtvtpkmlagfigskenhgqlisfeacmtqlyffligctecvll 120  
QY 121 AVMAVDYVAICHPPLHYPIYVSSRLCVQMAAGSWAGFGISMKVYKVELISRLSYCGPNTIN 180  
DB 121 avmaydryvaichpplhyvpyivssrlcvqmaagswagfgismkvkvelisrlsygcpntln 180  
QY 181 HFFCQVSPULNISCCTDMSTAEITDFVLAIFILGLPSTVGASYMAITGAVMRIPSAAGR 240  
DB 181 hffcdvspulniscctdmstaeltfdvllaifilglpstvgaasymaitgavmrpsaagrh 240  
QY 241 KAFSTCASHLTWVITFYVASTFIYARPKALSAFDNKLVSIVYAVIVPFFNFITICLRNQ 300  
DB 241 kafstcashltwvltfyvastsfiyarpkalsafdnklvsvlyavivpffnfiycltnq 300

QY 301 DVKRALRRTLHLAADOEANTNGSK 325  
:||||| ||||| : : :  
Db 301 evkralcctlnhlyqhgdpdkkaar 325

## RESULT 3

AAG71675  
ID AAG71675 standard; Protein: 327 AA.

AC AAG71675;

DT 31-JUL-2001 (first entry)

DE Human olfactory receptor polypeptide, SEQ ID NO: 1356.

KW Human: olfactory receptor; OR: primary scent determination;  
KW secondary scent determination; polypeptide library; odour receptor;  
KW scent profile; scent fingerprint; scent representation.

OS Homo sapiens.

PN W0200127158-A2.

PD 19-APR-2001.

PE 06-OCT-2000; 2000MO-US27582.

PR 08-OCT-1999; 990US-0158615.

PR 24-FEB-2000; 2000US-0184809.

PA (DIGI-) DIGISCENTS.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI: 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory  
sensation for identifying olfactory agonists and antagonists -

XX Claim 11: Page 839-840; 1857pp; English.

CC The present sequence is an olfactory receptor which is encoded by  
CC one of a number of novel polynucleotides. The polynucleotides can be  
CC used in screening for olfactory agonists and antagonists. The methods  
CC allow for the determination of primary scents and the identification  
CC of the odour receptors used to detect these primary scents. The methods  
CC also enable determination of secondary scents and the identification of  
CC combinations of odour receptors that are involved in detecting such  
CC secondary scents. This enables the construction of a scent representation  
CC (also called a scent fingerprint or scent profile), which may be used to  
CC re-create and edit scents. Libraries of olfactory receptors are useful  
CC for determining the interaction pattern of a composition with the  
CC receptors, and can be used for determining differences in the olfactory  
CC faculties of different individuals.

XX Sequence 327 AA;

Query Match 86.2%; Score 1454; DB 22; Length 327;

Best Local Similarity 88.7%; Pred. No. 1e-161;

Matches 282; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 8 GRVSEFVLGPPAPAPRVLFLSLDDYVLVTENMLIIIRNHTLTKPMFFLANM 67

Db 10 gexgetvllgfpapapivllfllaylvltencilimainhbsctlnhpmfflanm 69

QY 68 SFLFIWYVTPIPKMLAGFISKENHCOLISFEACMTOLYFELGLGCTECVLAWMAYDR 127

Db 70 sfletwytvtvripkmlagfysgskdqhlisfegcmqilyffliglgtcecvllawmaydr 129

QY 128 YVAICHLHPYIVIVSSRLCVOMAGSWGFGISMKVFLISRLSLGCPNTINHFFCDVS 187

Db 130 ymalcylhlypvlavsg-lcvqmaagswagfgislmvkvflisglsygpmlinhffcdvs 189

QY 188 PLNLSTDMSTALTFPVLAIFLLGLPLSYTGASVMAITGAVWRIRPSAAGRKAESTCA 247

Db 190 plnlscdtmstaeltfdlfflllplsvtgasyvaltgavnhlpsaagrykafstca 249

QY 248 SHLVVITFIYFAASIFITARPKAISAPDTNKLVSIVLAVIPLFNPITCYLRNOVKRALR 307

Db 250 shltvvlitfyaaasiflyarpkaalsafotnklvsvlyavivpllnllycltngdevkralc 309

QY 308 RTLHLAADOEANTNGSK 325

Db 310 cthlyqhgdpdkkaar 327

## RESULT 4

AAG71683  
ID AAG71683 standard; Protein: 327 AA.

AC AAG71683;

DT 31-JUL-2001 (first entry)

DE Human olfactory receptor polypeptide, SEQ ID NO: 1364.

KW Human: olfactory receptor; OR: primary scent determination;  
KW secondary scent determination; polypeptide library; odour receptor;  
KW scent profile; scent fingerprint; scent representation.

OS Homo sapiens.

PN W0200127158-A2.

PD 19-APR-2001.

PE 06-OCT-2000; 2000MO-US27582.

PR 08-OCT-1999; 990US-0158615.

PR 24-FEB-2000; 2000US-0184809.

PA (DIGI-) DIGISCENTS.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI: 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory  
sensation for identifying olfactory agonists and antagonists -

XX Claim 11: Page 846-847; 1857pp; English.

CC The present sequence is an olfactory receptor which is encoded by  
CC one of a number of novel polynucleotides. The polynucleotides can be  
CC used in screening for olfactory agonists and antagonists. The methods  
CC allow for the determination of primary scents and the identification  
CC of the odour receptors used to detect these primary scents. The methods  
CC also enable determination of secondary scents and the identification of  
CC combinations of odour receptors that are involved in detecting such  
CC secondary scents. This enables the construction of a scent representation  
CC (also called a scent fingerprint or scent profile), which may be used to  
CC re-create and edit scents. Libraries of olfactory receptors are useful  
CC for determining the interaction pattern of a composition with the  
CC receptors, and can be used for determining differences in the olfactory  
CC faculties of different individuals.

XX Sequence 327 AA;

Query Match 82.7%; Score 1395; DB 22; Length 327;

Best Local Similarity 85.5%; Pred. No. 8.6e-155;

Matches 272; Conservative 14; Mismatches 32; Indels 0; Gaps 0;

QY 8 GRVSEFVLLGFPAPADLRVLLFELSLDYLVTLENMLIIAIRNHPRLHKKPMYFEFLAMN 67  
 10 gegefvlilgfpapapilqylsfarsaayalvtentliimaarnhslhkpmlyfvlamm 69  
 Db 68 SFLEIYVVTITPKMLAGTIGSKENHGLISFEACMTQLYFLGLCTECVLLAVNAYDR 127  
 70 sstlelyvvtitpkmlagtgyskqdhqqlistegcmtdqlyflgltcecvllavmaydr 129  
 QY 128 YVAICHPHYVIVSSRLCYOMAGSMAGFGISMKVFEFLISRLSYCGPNTINHFECDVS 187  
 130 ymaicphlypivysgrlcyvmaagswagfgismvkvflisglsycgnpiinhffcdvs 189  
 Db 188 PLINISCTDMSTAEITDPEVLAIFILLGPLSVTCGASYMAITGAVMRIPSAAGRHAESTCA 247  
 190 pliniscdmstaeitdpevllaifillgplsvtcgasyvaltgavmhtsaagrykafstca 249  
 QY 248 SHLTWVITFYAASIFFYARPKALSAFDTNKIVSVLXAVIVPLFNPIIYCLRNODVRAIR 307  
 250 shltwviltfyaasiflyarpkalsafdtknkivsvlyavivplfnpiilyclrnqvkralc 309  
 QY 308 RFLHLAQDOEANTNKGSK 325  
 310 ctlhlyqhdpppkksr 327  
 Db  
 RESULT 5  
 AAR48744  
 ID AAR48744 standard; Protein; 286 AA.  
 AC AAR48744;  
 XX  
 DT 07-JUN-1996 (first entry)  
 DE G-protein coupled odorant receptor 17 protein.  
 XX  
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;  
 KW psychotonic disorder; schizophrenia; dopamine; CAMP; adenosine; thrombin;  
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;  
 KW rhodopsin; opsin; odorant; cytomagalovirus.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 9 \*/note= "unknown amino acid"  
 XX  
 PN WO9405695-A1.  
 XX  
 PD 17-MAR-1994.  
 XX  
 PF 09-SEP-1993; 93WO-US08528.  
 XX  
 PR 10-SEP-1992; 92US-0943236.  
 XX  
 PA (UYNV ) UNITV NEW YORK STATE.  
 XX  
 PI Murphy RB, Schuster DI;  
 XX  
 DR WPI, 1994-101120/12.  
 XX  
 PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for  
 binding GPR ligands or modulating GPR binding  
 PS  
 XX Disclosure: Page 120; 160pp; English.  
 CC Proteins AAR48685-R48758 represent a range of G-protein coupled receptor  
 CC proteins selected from CAMP, adenosine, muscarinic acetylcholine,  
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,  
 CC odorant, cytomagaloviral and other G-protein coupled receptors. The  
 CC receptor proteins were used to design polypeptides, pref. based on the  
 CC transmembrane domains, for use in G-protein coupled receptor ligand  
 CC binding assays. The polypeptide fragments retain biological activity

CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR  
 CC (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples  
 CC of polypeptide fragments). The polypeptide fragments can be used in  
 CC compositions for treating subjects suffering from a pathology related to  
 CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.  
 XX  
 SQ Sequence 286 AA:  
 Query Match 82.0%; Score 1382.5; DB 15; Length 286;  
 Best Local Similarity 91.7%; Pred. No. 2,1e-153;  
 Matches 276; Conservative 4; Mismatches 6; Indels 15; Gaps 4;  
 QY 27 LFEFLSLDYLVTLENMLIIAIRNHPRLHKKPMYFEFLAMNSFLEIYVVTITPKMLAGF 86  
 1 lfflsllykylvltlenmliiairnhprlhkpmlyffl----flslvvtitpklm-gf 55  
 Db  
 QY 87 IGSKENHGLISFEACMTQLYFLGLCTECVLLAVNAYDRVATCRPHRYIVSSRLC 146  
 56 lgskenhgqlisfcaemtdqlyflgltcecvllavmaydryvalchphlyvlyssrlz 115  
 Db  
 QY 147 VOMAGSMAGFGISMKVFEFLISRLSYCGPNTINHFECDVSPPLNLSCTDMSTAEITDPEV 206  
 116 v---lgsvaggfgismvkvflisrlyscgpnthffcdvspplnlsctdmstaeitdvt 172  
 Db  
 QY 207 LAIFILLGPLSVTCGASYMAITGAVMRIPSAAGRHAESTCASHLVIIIFYAASIFYAR 266  
 173 laifillgplsvtcgasymtgavmrripsaagrhaestcashlvviiifyaasifyar 225  
 Db  
 QY 267 PKALSAFDTNKIVSVLXAVIVPLFNPIIYCLRNODVRAIRLHLAQDOEANTNKGSKI 326  
 226 pkalsafdtknkivsvlyavivplfnpiilyclrnqvkraltlrlhlaqdqaentnkgski 285  
 Db  
 QY 327 G 327  
 286 g 286  
 Db  
 RESULT 6  
 ID AAM02716 standard; peptide; 286 AA.  
 XX  
 AC AAM02716;  
 XX  
 DT 13-NOV-1996 (first entry)  
 DE G-protein coupled odorant receptor 17.  
 XX  
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;  
 KW schizophrenia; dopamine; CAMP; adenosine; thrombin; adrenergic; opsin;  
 KW muscarinic acetylcholine; endocrine; bombesin; endocrine; rhodopsin;  
 KW odorant; cytomagalovirus; serotoninergic.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 9 /note= "unknown amino acid"  
 XX  
 PN US5508384-A.  
 XX  
 PD 16-APR-1996.  
 XX  
 PF 10-SEP-1992; 92US-0943236.  
 XX  
 PR 09-SEP-1993; 93US-0118270.  
 XX  
 PA 10-SEP-1992; 92US-0943236.  
 XX  
 PI (UYNV ) UNITV NEW YORK STATE..  
 XX  
 DR Murphy RB, Schuster DI;  
 XX  
 WPI, 1996-208785/21.

XX New dopamine receptor peptide - useful as antipsychotic agent, e.g.  
 PT for treating schizophrenia  
 XX  
 PS Disclosure; Column 153-156; 184pp; English.  
 XX  
 CC Proteins AAM02657-W02730 represent a range of G-protein coupled receptor  
 CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,  
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,  
 CC odorant, cytomegalo viral and other GPR proteins. The receptor proteins  
 CC were used to design polypeptides, pref. based on the transmembrane  
 CC domains, for use in G-protein coupled receptor ligand binding assays.  
 CC The polypeptide fragments retain biological activity such as binding a  
 CC GPR ligand or modulating GPR ligand binding to a GPR (see  
 CC AAM02747-W02999 for examples of polypeptide fragments). The polypeptide  
 CC fragments can be used in compositions for treating subjects suffering  
 CC from a pathology related to a GPR abnormality e.g. a psychotic disorder  
 CC such as schizophrenia.  
 CC  
 XX  
 SQ Sequence 286 AA;  
 82.0%; Score 1382.5; DB 17; Length 286;  
 Query Match Best Local Similarity 91.7%; Pred. No. 2.1e-153;  
 Matches 276; Conservative 4; Mismatches 6; Indels 15; Gaps 4;  
 QY 27 LLEFLSLDYLVLVTENMLIIAIRNPTLHKPMYFELANMSFLEIYVYVITIPKMLAGF 86  
 Db 1 ILLIISLIYVIVITENMLIIAIRNPTLHKPMYFELANMSFLEIYVYVITIPKMLAGF 55  
 QY 87 IGSKENHGQILSFECMTQLYFFELGLCTECVLAVMAYDRYVAICHPLHYPIVSSRLC 146  
 Db 56 IGSKENHGQILSFECMTQLYFFELGLCTECVLAVMAYDRYVAICHPLHYPIVSSRLC 115  
 QY 147 VQMAAGSMAGGFGISMKVFLISRLSCGPTINHFCDVSPILNCTDMSTAEITDFV 206  
 Db 116 V--IGSWAGGFGISMKVFLISRLSCGPTINHFCDVSPILNCTDMSTAEITDFV 172  
 QY 207 LAIFILGPTSVTGAVMATGAVMRIPSAAGRHKAFTSCASHLTVAITFYAASIFFYAR 266  
 Db 173 LAIFILGPTSVTGAVMATGAVMRIPSAAGRHKAFTSCASHLTVAITFYAASIFFYAR 225  
 QY 267 PKALSAEDTNKLVSVLAVIPLFNPIIYCLRNODVKRALRRLHLAODQEAANTNKGSKI 326  
 Db 226 PKALSAEDTNKLVSVLAVIPLFNPIIYCLRNODVKRALRRLHLAODQEAANTNKGSKI 285  
 QY 327 G 327  
 Db 286 g 286  
 RESULT 7  
 AAG72010  
 ID AAG72010 standard; Protein; 278 AA.  
 XX  
 AC AAG72010;  
 XX  
 DT 30-JUL-2001 (first entry)  
 XX  
 DE Human olfactory receptor polypeptide, SEQ ID NO: 1691.  
 XX  
 KW Human: olfactory receptor; OR: primary scent determination;  
 KW secondary scent determination; polypeptide library: odour receptor;  
 KW scent profile; scent fingerprint; scent representation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200127158-A2.  
 XX  
 PD 19-Apr-2001.  
 XX  
 PF 06-OCT-2000; 2000WO-US27582.  
 XX

PR 08-OCT-1999; 99US-0158615.  
 PR 24-FEB-2000; 2000US-0184809.  
 XX  
 PA (DIGI-) DIGISCENTS.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;  
 DR WPI; 2001-290713/30.  
 XX  
 PT New polynucleotides which encode polypeptides involved in olfactory  
 PT sensation for identifying olfactory agonists and antagonists -  
 PS Claim 11; Page 1102-1103; 1857pp; English.  
 XX  
 CC The present sequence is an olfactory receptor which is encoded by  
 CC one of a number of novel polynucleotides. The polynucleotides can be  
 CC used in screening for olfactory agonists and antagonists. The methods  
 CC allow for the determination of primary scents and the identification  
 CC of the odour receptors used to detect these primary scents. The methods  
 CC also enable determination of secondary scents and the identification of  
 CC combinations of odour receptors that are involved in detecting such  
 CC secondary scents. This enables the construction of a scent representation  
 CC (also called a scent fingerprint or scent profile), which may be used to  
 CC re-create and edit scents. Libraries of olfactory receptors are useful  
 CC for determining the interaction pattern of a composition with the  
 CC receptors, and can be used for determining differences in the olfactory  
 CC faculties of different individuals.  
 CC  
 XX  
 SQ Sequence 278 AA;  
 74.0%; Score 1248; DB 22; Length 278;  
 Query Match Best Local Similarity 87.4%; Pred. No. 1.2e-137;  
 Matches 243; Conservative 13; Mismatches 22; Indels 0; Gaps 0;  
 QY 48 IAIRNPTLHKPMYFELANMSFLEIYVYVITIPKMLAGFISKENHGQILSFECMTQLY 107  
 Db 1 IAIRNPTLHKPMYFELANMSFLEIYVYVITIPKMLAGFISKENHGQILSFECMTQLY 60  
 QY 108 FFLGLGCTECVLAVMAYDRYVAICHPLHYPIVSSRLCQVMAAGSMAGGFGISMKVFL 167  
 Db 61 FFLGLGCTECVLAVMAYDRYVAICHPLHYPIVSSRLCQVMAAGSMAGGFGISMKVFL 120  
 QY 168 ISRLSCGPTINHFCDVSPILNCTDMSTAEITDFVLAIFILGPTSVTGAVMAT 227  
 Db 121 ISRLSCGPTINHFCDVSPILNCTDMSTAEITDFVLAIFILGPTSVTGAVMAT 180  
 QY 228 GAVMRIPSAAGRHKAFTSCASHLTVAITFYAASIFFYARPKALSAEDTNKLVSVLAVI 287  
 Db 181 GAVMRIPSAAGRHKAFTSCASHLTVAITFYAASIFFYARPKALSAEDTNKLVSVLAVI 240  
 QY 288 PLFNPIIYCLRNODVKRALRRLHLAODQEAANTNKGSK 325  
 Db 241 PLFNPIIYCLRNODVKRALRRLHLAODQEAANTNKGSK 278  
 RESULT 8  
 AAG72365  
 ID AAG72365 standard; Protein; 278 AA.  
 XX  
 AC AAG72365;  
 XX  
 DT 30-JUL-2001 (first entry)  
 XX  
 DE Human OR-like polypeptide query sequence, SEQ ID NO: 2046.  
 XX  
 KW Human: olfactory receptor; OR: primary scent determination;  
 KW secondary scent determination; polypeptide library: odour receptor;  
 KW scent profile; scent fingerprint; scent representation.  
 XX  
 OS Homo sapiens.  
 XX

PM WO200127158-A2.  
XX  
PD 19-APR-2001.  
XX  
XX 06-OCT-2000; 2000WO-US27582.  
PF  
XX 08-OCT-1999; 99US-0158615.  
PR 24-FEB-2000; 2000US-0184809.  
XX  
XX (DIGI-) DIGISCENTS.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
XX  
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;  
XX  
XX WPI: 2001-290713/30.  
DR  
XX  
XX New polynucleotides which encode polypeptides involved in olfactory  
PT sensation for identifying olfactory agonists and antagonists -  
PT  
XX  
XX Example 6; Page 1371-1372; 1857pp; English.  
PS  
XX  
XX The present sequence is a polypeptide encoded by one of 344 newly mined  
CC human genes. It was used as a query sequence in a database search of  
CC olfactory receptor (OR)-like sequences. The invention relates to isolated  
CC polynucleotides encoding polypeptides involved in olfactory sensation.  
CC The polynucleotides can be used in screening for olfactory agonists and  
CC antagonists. The methods allow for the determination of primary scents  
CC and the identification of the odour receptors used to detect these  
CC primary scents. The methods also enable determination of secondary scents  
CC and the identification of combinations of odour receptors that are  
CC involved in detecting such secondary scents. This enables the  
CC construction of a scent representation (also called a scent fingerprint  
CC or scent profile), which may be used to re-create and edit scents.  
CC Libraries of olfactory receptors are useful for determining the  
CC interaction pattern of a composition with the receptors, and can be  
CC used for determining differences in the olfactory faculties of different  
CC individuals.  
XX  
XX Sequence 278 AA:  
SQ  
Query Match 74.0%; Score 1248; DB 22; Length 278;  
Best Local Similarity 87.4%; Pred. No. 1,2e-137;  
Matches 243; Conservative 13; Mismatches 22; Indels 0; Gaps 0;  
QY 48 IAINRHPPLHMKPMYFFELANMSELEIYVTVTPKMLAGFSGKENHGQLISFEACMTOLY 107  
DB 1 mairnhtshkpmgyfflaamsfleiwyvvtlpmklagfsgkqhgqlisfegcmtdly 60  
QY 108 PFLGAGCTECVLLAVMAVDRYVAICHPLHYPIYVSSRLCVQMAAGSMAGFGTSMWKVL 167  
DB 61 flfigagctecvllavmandryvalmaicylhnpvlysgrlcvqmaagsgwagfigismwkvfl 120  
QY 168 ISRLSYCGPNTNHFECDDVSPILNLSCTDMSTAEILDVLAIFILLGPSTVGASGMAT 227  
DB 121 lsglsgnspnlhntfcdvspilnlsctdmstaeiltfdllaifillgpstvgasgmat 180  
QY 228 GAVMRIPSAAGRHKAFCSCASHLTAVIIFYASIFIRAPKALSAFDTNKLVSVLAVIV 287  
DB 181 gavmripaagrykafscashltaviflyasifirapkalasfdtnklvsylvaviv 240  
QY 268 PLENPITICLRQDVKRALRRTLHLAQQDOEANTNKGSK 325  
DB 241 pllnpilycltrngvkrallcccllhynqdpdkkgsr 278

XX  
DE Human olfactory receptor AOLF221.  
XX  
XX Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;  
KW food additive; cosmetic; fragrance; pharmaceutical additive.  
XX  
XX Homo sapiens.  
XX  
XX WO200168805-A2.  
XX  
XX  
XX 20-SEP-2001.  
XX  
XX  
XX 13-MAR-2001; 2001WO-US07771.  
XX  
XX 13-MAR-2000; 2000US-0188914.  
XX 24-MAR-2000; 2000US-0192033.  
XX 12-APR-2000; 2000US-0198474.  
XX 26-APR-2000; 2000US-0199335.  
XX 26-MAY-2000; 2000US-0207702.  
XX 23-JUN-2000; 2000US-0213849.  
XX 16-AUG-2000; 2000US-0226534.  
XX 07-SEP-2000; 2000US-0230732.  
XX 07-FEB-2001; 2001US-0266862.  
XX  
XX (SENO-) SENOMTX INC.  
XX  
XX Zozulya S;  
XX  
XX WPI: 2001-570867/64.  
XX N-PSDB; AAS42415.  
DR  
XX  
XX Nucleic acids encoding human olfactory G protein-coupled receptors,  
PT useful for screening for compounds involved in olfactory sensation,  
PT where the compounds can be used in the food, pharmaceutical and  
XX cosmetic industries to customise odours -  
XX  
XX  
XX Claim 60; Page 176; 319pp; English.  
PS  
XX  
XX  
XX The invention relates to nucleic acids encoding human olfactory  
CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's  
CC specifically recognise molecules, odourants, that elicit specific  
CC olfactory sensation. The human olfactory receptors and polynucleotides  
CC encoding them are useful for screening a library of chemical compounds  
CC for compounds that are involved in olfactory sensation. Modulators of  
CC their activity are useful for pharmacological and genetic modulation of  
CC olfactory signalling pathways. Therefore, they can be used in the food,  
CC pharmaceutical and cosmetic industries to customise odours and  
CC fragrances. The present sequence is a human olfactory receptor of the  
CC invention.  
XX  
XX  
XX Sequence 317 AA:  
SQ  
Query Match 57.6%; Score 971.5; DB 22; Length 317;  
Best Local Similarity 57.1%; Pred. No. 3.8e-105;  
Matches 181; Conservative 55; Mismatches 72; Indels 9; Gaps 3;  
QY 4 RNHS-GRVSEFVLGFPAPAPRLVFLFLSLDYLVTENMLIIAIRNHPPLHMKPMYF 62  
DB 2 nlsqsgnheeflvqfptcpqlilflvlfaiylltllenllyfttlwapslnrmpyf 61  
QY 63 FLANMSFLEIYVTVTPKMLAGFSGKENHGQLISFEACMTOLYFPLGAGCTECVLLAV 122  
DB 62 flghlsflelwyinvtlpillafl----tgdgrvsyvgcmtdlyfflallactecvllav 117  
QY 123 MAYDRYVAICHPLHYPIYVSSRLCVQMAAGSMAGFGTSMWKVLISRLSYCGPNTNHF 182  
DB 118 maydrylaicgpllypslmpsslacrlaasvsgsfssmmllfltsqlyscgpnllhntf 177  
QY 183 FCDVSPILNLSCTDMSTAEILDVLAIFILLGPSTVGASGMATGAVMRIPSAAGRHKA 242  
DB 178 fcdvspilnlsctdmstaeltdvllaifillgpstvgasgmattgavmrripsaagrha 237



	Query Match	Similarity	Best Local	Matches	Conservative	Mismatches	Indels	Gaps
	57.5%	Score 970.5	DB 22	Length 313				
		58.1%	Pred. No. 4.9e-105					
				179	54	70	5	2
OY	4	RHHS - GRSEFVLLGEPAPARLVLLFLSLDDYVYVLTENMLIIITAIIRNHPPLKHPMF	62					
Db	2							
OY	63	FLANNSFLFIWVYVVIIPMLAGTIGSKENHQQLISFEACQTLVYFLGLGCTECVLLAV	122					

RESULT	11
AA66357	
ID	AA66357 standard; Protein; 301 AA.
XX	
AC	AA66357;
XX	
DT	15-OCT-2001 (first entry)
XX	
DE	Human olfactory receptor C6 partial protein.
XX	
KW	NOY; olfactory; cytosolic; immunomodulator; vulnereary; anti-HIV;
KW	antiallergic; antiinflammatory; gastrointestinal; neuroprotective;
KW	osteopathic; gene therapy; odorant receptor; olfactory receptor;
KW	G-protein coupled receptor; GPCR; neuro-olfactory; trauma; human;
KW	neoplastic disorder; cancer; adenocarcinoma; lymphoma; prostate cancer;
KW	uterus cancer; immune response; AIDS; asthma; Crohn's disease;
KW	multiple sclerosis; Albright hereditary osteodystrophy.
XX	
OS	Homo sapiens.
XX	
PN	WO200155179-A2.
XX	
PD	02-AUG-2001.
XX	
PF	29-JAN-2001; 2001WO-US02849.
XX	
PR	27-JAN-2000; 2000US-0178370.
XX	
PR	27-JAN-2000; 2000US-0178371.
PR	27-JAN-2000; 2000US-0178406.
PR	27-JAN-2000; 2000US-0178408.
PR	27-JAN-2000; 2000US-0178409.
PR	27-JAN-2000; 2000US-0178413.
PR	27-JAN-2000; 2000US-0178414.
PR	07-FEB-2000; 2000US-0180634.
PR	24-JUL-2000; 2000US-0220516.
PR	28-JUL-2000; 2000US-0221408.
PR	31-JUL-2000; 2000US-0221943.
PR	21-DEC-2000; 2000US-0257599.
PR	08-JAN-2001; 2001US-0260290.
XX	
PA	(CUBA-) CUBAGEN CORP.
XX	
PI	Prayaga SK, Padigaru M, Spytek KA, Li L, Tchernev VT, Vernet CM;
PI	Peyman JA, Macdougall J,
XX	
DR	WPI: 2001-514556/56.
XX	
XX	
PT	New NOYX polypeptides and polynucleotides, useful for treating or
PT	preventing a syndrome associated with a human disease (e.g. disorders
PT	of the neuro-olfactory system), as well as in gene therapy -
XX	
PS	Disclosure: Page 58; 242pp; English.
XX	
CC	The present invention relates to novel human NOYX proteins and coding



PN WO200127158-A2.  
XX  
PD 19-APR-2001.  
XX  
PF 06-OCT-2000; 2000WO-US27582.  
XX  
PR 08-OCT-1999; 99US-0158615.  
PR 24-FEB-2000; 2000US-0184809.  
XX  
PA (DIGI-) DIGISCENTS.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
XX  
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;  
XX WPI; 2001-290713/30.  
XX  
PT New polynucleotides which encode polypeptides involved in olfactory  
PT sensation for identifying olfactory agonists and antagonists -  
XX  
XX Example 6; Page 1368-1369; 1857pp; English.  
XX  
XX The present sequence is a polypeptide encoded by one of 344 newly mined  
CC human genes. It was used as a query sequence in a database search of  
CC olfactory receptor (OR)-like sequences. The invention relates to isolated  
CC polynucleotides encoding polypeptides involved in olfactory sensation.  
CC The polynucleotides can be used in screening for olfactory agonists and  
CC antagonists. The methods allow for the determination of primary scents  
CC and the identification of the odour receptors used to detect these  
CC primary scents. The methods also enable determination of secondary scents  
CC and the identification of combinations of odour receptors that are  
CC involved in detecting such secondary scents. This enables the  
CC construction of a scent representation (also called a scent fingerprint  
CC or scent profile), which may be used to re-create and edit scents.  
CC Libraries of olfactory receptors are useful for determining the  
CC interaction pattern of a composition with the receptors, and can be  
CC used for determining differences in the olfactory faculties of different  
CC individuals.  
XX  
XX Sequence 311 AA;  
SQ

Query Match 56.8%; Score 957.5; DB 22; Length 311;  
Best Local Similarity 56.8%; Pred. No. 1.6e-103;  
Matches 175; Conservative 54; Mismatches 72; Indels 7; Gaps 3;

QY 1 MERNHSGRSEFVLGFPAPARVLLFSLLDYVLVLENNLIIAIRNHTLAKPM 60  
DB 1 melenql-rvklkllvgfpgslsmraamflilvaylllvaenvllllvlnqrpnlkpm 59  
XX  
QY YFPLANSPLEIWTYVTPKMLAGTSGKENHGQLISFEACMTQLYFFLGCTCEVL 120  
DB 60 yfllanlsfletwyistvtpkllfsfswms----isfclcmqllyffllalmtecvll 115  
XX  
QY 121 AVMAVDRYVAICHPPLHVPVIVSSRLCYOMAGSWAGFGISMWKVFILSRLSYCGPMTIN 180  
DB 116 aamaydyvaicrpllhvptlmsbqlcfrlalswaigfislaklyfiscisfcgpnvln 175  
XX  
QY 181 HFECDSVPLNLSTCTDMSTELDFVLAIFLLGPLSVTGASVMAITGAVWRIPSAGR 240  
DB 176 hfcdslspvnlstctdmstelmtefvlalvlfllpflfvlsvygcclatlcmpt--gkq 233  
XX  
QY 241 KAFSTCASHLTUVLIIFVAASIFIVARPKALSAFTNKLVSALVAVIPLFNPIIYCLRNQ 300  
DB 234 kafstcshltuvlviifvaasifivarpkalsafntklnvslavaviplfnpiiyclrnq 293  
XX  
QY 301 DVKRALRR 308  
DB 294 evkealkk 301  
XX

RESULT 14  
AAG71590  
ID AAG71590 standard; Protein: 324 AA.

XX  
AC AAG71590;  
XX  
DT 30-JUL-2001 (first entry)  
XX  
DE Human olfactory receptor polypeptide, SEQ ID NO: 1271.  
XX  
XX Human: olfactory receptor; OR: primary scent determination;  
KM secondary scent determination; polypeptide library; odour receptor;  
KM scent profile; scent fingerprint; scent representation.  
XX  
XX Homo sapiens.  
XX  
PN WO200127158-A2.  
XX  
PD 19-APR-2001.  
XX  
PF 06-OCT-2000; 2000WO-US27582.  
XX  
PR 08-OCT-1999; 99US-0158615.  
PR 24-FEB-2000; 2000US-0184809.  
XX  
PA (DIGI-) DIGISCENTS.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
XX  
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;  
XX WPI; 2001-290713/30.  
XX  
PT New polynucleotides which encode polypeptides involved in olfactory  
PT sensation for identifying olfactory agonists and antagonists -  
XX  
XX Claim 11; Page 770-771; 1857pp; English.  
PS  
XX  
XX The present sequence is an olfactory receptor which is encoded by  
CC one of a number of novel polynucleotides. The polynucleotides can be  
CC used in screening for olfactory agonists and antagonists. The methods  
CC allow for the determination of primary scents and the identification  
CC of the odour receptors used to detect these primary scents. The methods  
CC also enable determination of secondary scents and the identification of  
CC combinations of odour receptors that are involved in detecting such  
CC secondary scents. This enables the construction of a scent representation  
CC (also called a scent fingerprint or scent profile), which may be used to  
CC re-create and edit scents. Libraries of olfactory receptors are useful  
CC for determining the interaction pattern of a composition with the  
CC receptors, and can be used for determining differences in the olfactory  
CC faculties of different individuals.  
XX  
XX Sequence 324 AA;  
SQ

Query Match 56.08%; Score 944.5; DB 22; Length 324;  
Best Local Similarity 57.28%; Pred. No. 5.6e-102;  
Matches 178; Conservative 54; Mismatches 74; Indels 5; Gaps 2;

QY 1 MERNHSGRSEFVLGFPAPARVLLFSLLDYVLVLENNLIIAIRNHTLAKPM 60  
DB 6 levnhnt-vtrfllilgfpctpaqgllffsfiflatytlitlenllllahsogqlkpm 64  
XX  
QY YFPLANSPLEIWTYVTPKMLAGTSGKENHGQLISFEACMTQLYFFLGCTCEVL 120  
DB 65 yfllshlsflemwyvvtvlsipkmlvdfll----shdksisfngcmqllyffvtvcteylll 120  
XX  
QY 121 AVMAVDRYVAICHPPLHVPVIVSSRLCYOMAGSWAGFGISMWKVFILSRLSYCGPMTIN 180  
DB 121 aimafrdyvaicrpllhvptlmsbqlcfrlalswaigfislaklyfiscisfcgpnvln 180  
XX  
QY 181 HFECDSVPLNLSTCTDMSTELDFVLAIFLLGPLSVTGASVMAITGAVWRIPSAGR 240  
DB 181 hfcdslspvnlstctdmstelmtefvlalvlfllpflfvlsvygcclatlcmpt--gkq 240  
XX  
QY 241 KAFSTCASHLTUVLIIFVAASIFIVARPKALSAFTNKLVSALVAVIPLFNPIIYCLRNQ 300  
DB 241 kafstcshltuvlviifvaasifivarpkalsafntklnvslavaviplfnpiiyclrnq 300  
XX

Db 241 kafstcaashlevallfysmllfyparpkmyaaynskvsvlylvivplllmpilyclrn 300

Qy 301 DVKRALRRLTlh 311 .

Db 301 evkaalrktlh 311

RESULT	15
AAG72479	
ID	AAG72479 standard; Protein; 324 AA

AC AAG72479;

DT 30-JUL-2001 (first entry)  
xx

DE	Human OR-1-like polypeptide query sequence, SEQ ID NO: 2160.
----	--

KW Human; olfactory receptor; OR; primary scent determination;  
 KW secondary scent determination; polypeptide library; odour receptor  
 KW scent profile; scent fingerprint; scent representation.

OS Homo sapiens.

PN W0200127158-A2.

PD 19-APR-2001.

PF 06-OCT-2000; 2000WO-US27582.

PR 08-OCT-1999; 99US-0158615.

PR 24-FEB-2000; 2000US-0184809.

PA (DIGI-) DIGISCENTS.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I, ...

DR WPI; 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory  
PT sensation for identifying olfactory agonists and antagonists -

PS Example 6; Page 1452-1453; 1857pp; English.

The present sequence is a polypeptide encoded by one of 344 newly mined human genes. It was used as a query sequence in a database search of olfactory receptor (OR)-like sequences. The invention relates to isolated polynucleotides encoding polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals.

Sequence 324 AA;

Query Match	Score	DB	Length
56.08;	944.5;	22;	324;

QY 1 MERRNHSGRVSEFVLLGEPAPAPLRVLLFELSLDYVLTENMLIIAIRNHPTLHKPM 600

[illegible]

Search completed: May 22, 2002, 15:40:00  
Job time: 1251 sec